## STIC-Biotech/ChemLib

From:

Ton, Thaian

Sent:

Monday, May 20, 2002 9:41 AM

To: Cc:

STIC-Biotech/ChemLib

Subject:

Ton, Thaian Sequence Search Request

I would like to request a search for Application No. 09/696,686 [Inventor: Allen, Filing Date: 10/26/2000]

A standard sequence search for SEQ ID NOS: 45, 46, 47, 50 and 51 against the commercial nucleic acid databases.

Thank you very much.

Thaian N. Jon

Patent Examiner

Art Unit 1632

Room 12A16 CM1

Mailbox: 12E12 CM1

(703) 305-1019

of Contact: Sheppard

Phone: Location: \_ Date Picked Up: Date Completed: 5/25/02 Searcher Prep/Review: \_\_\_\_ Clerical: \_ Online time: \_\_\_\_

TYPE OF SEARCH:

NA Sequences:\_\_\_\_\_ AA Sequences:\_\_\_\_\_

Structures: \_

Bibliographic: Litigation: \_\_\_\_

Full text: Patent Family:\_\_\_\_\_ Other:

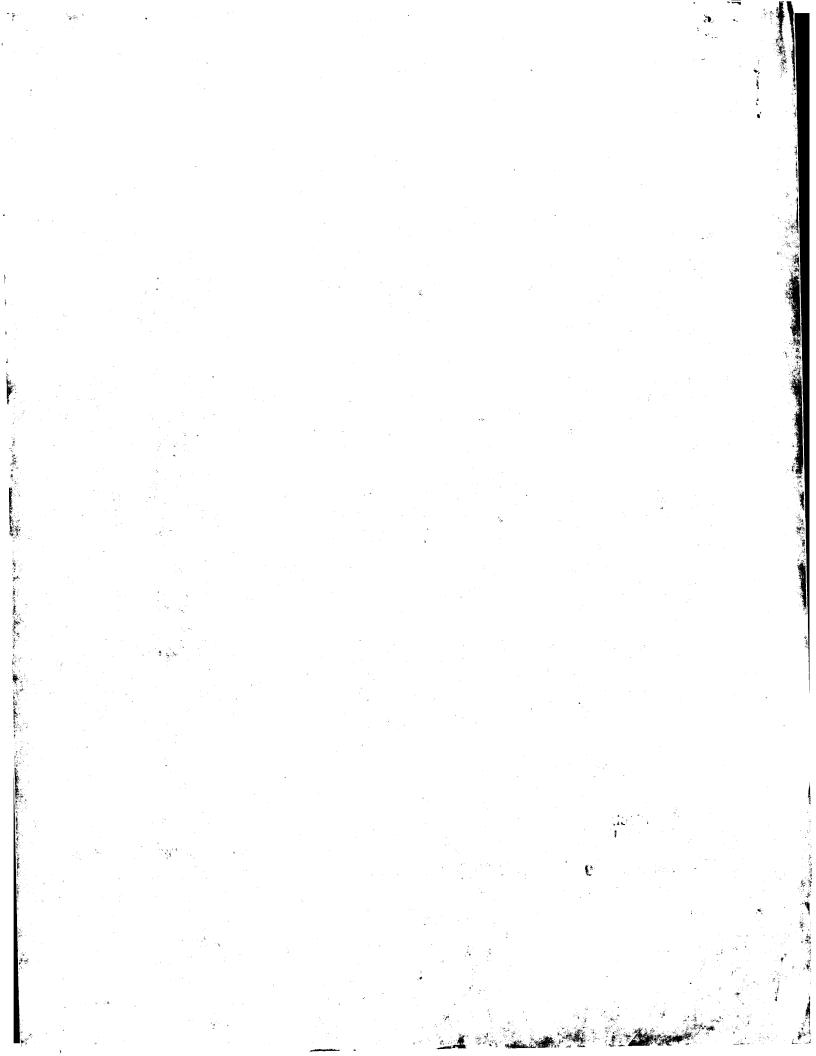
VENDOR/COST(where applic.)

STN: DIALOG:

Questel/Orbit: \_\_\_\_\_ DRLink:\_\_\_\_

Lexis/Nexis: Sequence Sys.: \_\_\_\_ WWW/Internet:

Other (specify):



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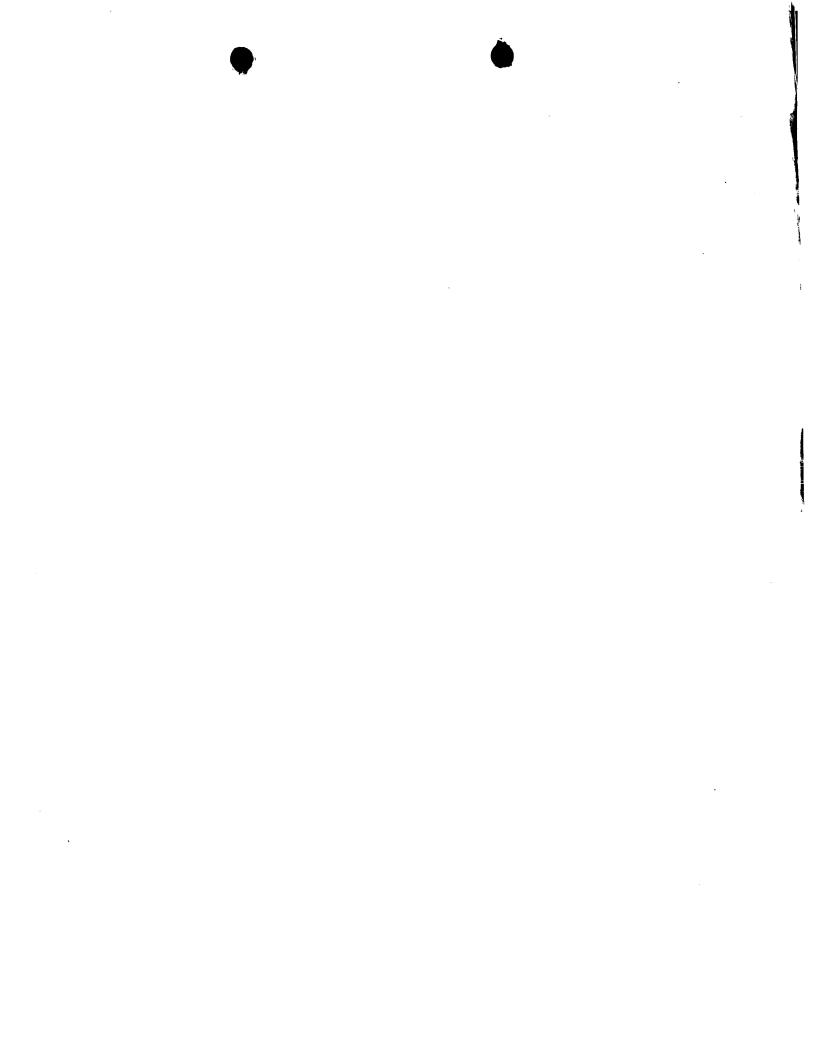
Patent Examiner

Art Unit 1632

Room 12A16 CM1

Mailbox: 12E12 CM1

(703) 305-1019



AL292874 Terreodon BG175514 602328165 AL052513 Drosophil AL106024 Drosophil B21793 F7E19-Sp6 I AL30040 Terraodon AC199361 Terraodon AG081192 Pan trogl BF256498 HVSMEf001

AG127829 Pan trool
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AL419809 TV end of
AL619809 TV end of
AL619809 TV end of
AL635833 AL535833
AG076623 Pan trool
AL13063 Pan trool
BM475329 AGENCOURT
AC132063 Pan trool
BM475329 AGENCOURT
AC132065 Pan trool
BG786306 SEAUMCOO6
AG049269 Pan trool
BH254587 Pan trool
BH254587 SALK\_0168
AG13186 Pan trool
BH254587 SALK\_0168
AG13186 Pan trool

Sequence:

Run on:

Searched:

Database

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AG128386.1 GI:16657551
GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC Library clone:PTB-139113.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AG128386 1090 bp DNA linear GSS 04-NOV-2001 Pan troglodytes DNA, clone: PTB-139113.R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Our Direct Submass 1 to 1080)

Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totocki, Y., Watanabe, H. and Sakaki, Y.

Totocki, Y., Watanabe, H. and Sakaki, Y.

Direct Submission

Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

and Chemical Research (RIKEN), Genomic Sciences Conter (GSC);

I-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)

Clonnes are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
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                                                                CNSOLSXA
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                                                                                                May 23, 2002, 23:06:04; Search time 4203.75 Seconds (Without alignments) 1187.957 Million cell updates/sec
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AL104537 T3 end of
AL106944 Drosophil
AZ184008 SP_1002_A
BF256755 HVSMEF001
AG126129 Pan trog1
AZ196637 SP_1037_B
AL072271 Drosophil
BE344494 ht69912.x
AO738512 HS_5381_B
BG52030 ps29b11.y
BI416482 hasp0lnx
AL071731 Drosophil
AL418302 T7 end of
BH021826 GH_MBb00
AG127831 Pan trog1
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     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                              OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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1. .1090 /organism="Pan troglodytes" /db\_xref="taxon:9598" /clone="PTB-139113.R"

Location/Qualifiers

source

CNSO6WDK BH021826 AG127831

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FEATURES

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Query Match
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This GSS is part of a random genomic sequencing program of thirteen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSS 17-JUN-2001
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341 bp DNA linear GSS 17-JUN-200
T3 end of clone AT0AA016H10 of library AT0AA from strain CBS 4311
of Saccharomyces servazzii, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G., Souciet, J.L., Aigle, M., Artiguenave, F., Casaregola, S., Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., Bolotin-Fukuhara, M., Durrens, P., Lepingle, A., Llorente, B., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S., Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J.
Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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Casaregola,S., Lepingle,A., Bon,E., Neuveglise,C., Nguyen,H., Artiguenave,F., Wincker,P. and Gaillardin,C.
Genomic exploration of the hemiascomycetous yeasts: 7.
Saccharomyces servazzii
FEBS Lett. 487 (1); 47-51 (2000)
                                                                                                                                                      Gaps
                                                                                                                                                                                    874 GGGGGGGGGGGGGGGGGGGGGGGGGGGGAAATGNGAAANAGGGAAAGGGAAGGGAA
                                                                                                                                                      ;
                                                                                                                 Length 1090;
              /cell_type="lymphoblast" /clone_lib="PTB Chimpanzee Male BAC Library" /clone_lib="PTB Chimpanzee Male BAC Library" 34 c 777 g 20 t 148 others
                                                                                                                                                      Indels
                                                                                                                       DB 12;
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                                                                                                                                       Pred. No. 0.31;
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ilarity 41.7%;
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/sex="male"
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Drosophila melanogaster genome survey sequence T7 end of BAC BACN16C14 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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                years spectracomyces servazzii, zygosaccharomyces rouxii, saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces tactis var. lactis, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces maxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
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Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
species: Saccharomyces bayanus var. uvarum, Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : : : | : | | | | | : | 314 KGGKKKRARGGKGGKKGTTRKGGKCKGGSKTCGKATTAATGAR 255
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                374 GKGGGTSGKGGKGGGGGGGGGGGCRGGGKKSGGGACAGRSAGGKAKAKGKRTTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62; Mismatches 151; Indels
                                                                                                                                                                                                                                                                                      /organism="Saccharomyces servazzii"
/strain="CBS 4311"
/db_xref="taxon:27293"
/clone_latoha016H10"
/clone_lib="ATOAA016H10"
/note="end: T3"
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32.8%; Pred. No. 0.4;
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library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Strongylocentrotus purpuratus
Eukaryota, Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinodea; Echinod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 cggggcctgtgggaagggtctgggcctggcaggacctgggctggggtctccttggcctg 135
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Proc. Natl. Acad. Sci. U. S. A. 97 (17), 9514-9518 (2000)
20402566
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                                                                                                                                                                                                                                                                                                                                                                                                     233 others
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                                                                                                                                                                                                         /organism="Drosophila melanogaster"
/plasmid="pBeloBAC11"
/db_xref="Laxon:7227"
/clone_lib="DrosBAC"
/clone="BACN16C14"
/note="end: T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.5%; Score 49.8; DB 12;
42.0%; Pred. No. 0.62;
Live 23; Mismatches 151;
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                                                                                                                                                         Location/Qualifiers
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Plate: 1002 row: G column
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Best Local Similarity 42.01
Matches 126; Conservative
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barley.

Hordeum vulgare

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta: Magnollophyta; Liliopsida: Poales; Poaceae; Pooldeae

Triticaes; Hordeum.

Triticaes; Hordeum.

Y. Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D. W., Fenton

Development of a genetically and physically anchored EST resource

for barley genomics: Morex unstressed seedling root cDNA library

On Nov 16, 2000 this sequence version replaced gi:11185868.
                                                                              /organism="Strongylocentrotus purpuratus"
//db_xref="taxon.7668"
//clone="Plate=1002 Col=6 Row=G"
//clone=lib="Strongylocentrotus purpuratus, purple sea
//clone=lib="Strongylocentrotus purpuratus, purple sea
//clone=lib="Strongylocentrotus purpuratus, purple sea
//note="Organ: Sperm; Vector: BACe3.6; BAC Clones in E-Coll
DH108"
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                                                                                                                                                                                                                                                                            Length 723;
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Pred. No. 0.61;
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clemson University
100 Jordan Hall, Clemson, SC 29634, US
Tel: 864 656 4293
Fax: 864 656 4293
Emall: rwing@clemson.edu
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                          High quality sequence stop: 723.
Location/Qualifiers
1. 723
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High quality sequence stop: 1129.
Location/Qualifiers
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                                                                                                                                                                                                                                                         13.4%; Scor.
48.5%; Pred
0; }
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BF256755.2 GI:16315528
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Matches 112; Conservative
Seq primer: SP6
Class: BAC ends
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Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical Submitted (02-AUG-2001), Genomic Sciences Center (GSC); and Chemical Research (RIKEN), Genomic Sciences Center (GSC); (E-mail:chimpbes@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Toliones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 660)
Cameron, R. A., Mahairas, G., Rast, J. P., Martinez, P., Biondi, T.R.,
Swartzell, S., Wallace, J. C., Poustka, A.J., Livingston, B.T., Wray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SP_1037_B2_F11_SP6E Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus genomic clone Plate=1037 Col=22 Row=L, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     139 tgtgctttgcggcaatgctgggtgctgtgactctcggataacctggagatccctgctttt 198
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Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
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       Taylor, T.D., Yada, T.,
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Pred. No. 0.78;
0; Mismatches 124;
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/db_xref="taxon:9598"
/clone="PTB-136J13.F"
          Fujiyama, A., Hattori, M., Toyoda, A., Totoki, Y., Watanabe, H. and Sakaki, Y. BAC end sequences of Library PTB Unpublished
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GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC Library clone:PTB-136J13.F.
Pan troglodytes
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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Pan troglodytes DNA, clone: PTB-136J13.F, genomic survey sequence.
AG126129
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/clone="HYSME010017"
/clone_ib="Hordeum vulgare seedling root EST library
HVcDNA0007 (Etiolated and unstressed)"
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Pred. No. 0.77;
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/lab_host="TJC121"
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47.8%;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                          /clone="Plate=1037 Col=22 Row=L"
/clone_lib="Strongylocentrotus purpuratus, purple sea
urchin, sperm genomic BAC library"
/note="Organ: sperm; Vector: BACe3.6; BAC Clones in E-Coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosopilla melanogaster genome survey sequence T7 end of BAC: BACR33010 of RPCI-98 library from Drosophila melanogaster (fruit AL072271
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Ettensohn, C.A., Lehrach, H., Britten, R.J, Davidson, E.H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : bp 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and
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                              urchin genome project: Sequence scan, virtual map, and
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Drosophila melanogaster
Eukaryota, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Proc. Natl. Acad. Sci. U. S. A. 97 (17), 9514-9518 (2000)
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/db_xref="taxon:7668"
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55.6%; Pred. No. 0.8;
11ve 0; Mismatches 68
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                                                                                                Contact: Cameron, RA, Davidson, EH Division of Biology 156-29
California Institute of Technology Basadena California 91125, USA Tel: (626) 395-8421
Fax: (626) 793-3047
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High quality sequence stop: 660.
Location/Qualifiers
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Plate: 1037 row: L column: 22
Seq primer: SP6
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Hood, L.
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When the standard of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutovyo Osogawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-B and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's PI and EST libraries. A more detailed description of the library
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Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, Wir. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2, cn bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segrefégenoscope.cns.fr
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/db_xxef="texon:7227"
/clone_lib="RPCI-98"
/clone="BACR33010"
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL, send email to:

info@inage.llnl.gov

Seq primer: -40UP from Gibco

High quality sequence stop: 457.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BE348494 11NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3152038 3' similar to contains element MSR1 repetitive element ; mRNA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 458)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

Tanional Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                              and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                      78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137 ICTAGATGGGGAGAGTCTKGGGGGGGTGTGGGGGRTKKGSGGTKGGGTKTGGTTGGGCG
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                                                                                                                                                                                                                                                 Length 295;
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                                                                                              melanogaster'
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                                                                                                                                                                                                                                                       DB 12;
                                                                                                                                                                                                                                                                                      14; Mismatches 116;
                                                                                                                                                                                                                                                     Score 48.4; DB 
Pred. No. 0.88;
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/tissue_type="carcinoid"
/lab_host="DH108"
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/clone="IMAGE:3152038"
                                                                                          /organism="Drosophila mk/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR29P06"
/note="end : T7"
a 200 c 5 9 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence.
BE348494
BE348494.1 GI:9260347
                                                                                                                                                                                                                                                       Query Match 13.1%;
Best Local Similarity 45.6%;
Matches 109; Conservative 1
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BE348494/c
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Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
701: (206) 616-3818
Fax: (206) 616-3818
Fax: (206) 616-3831
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Library availablility, please contact Pieter de Jong
library availablility, please contact Pieter de Jong
library availace.ubffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu,ordering_bac.htm)
ACPAC Resources (http://bacpac.med.buffalo.edu,ordering_bac.htm)
PACPAC Resources (http://www.htsc.washington.edu
Plate: 957 row: D column: 21
Seq primer: T7
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/note="Organ: lung: Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_Lu5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1414920-1417991 and 1520904-152439). Subtraction by Bento Soares and M. Fatima Bonaldo.

a 313 c 22 g 0 t 123 others
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bummalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 843)

Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,

Reller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. a.
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HS_5381_B1_B11_T7A RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=957 Col=21 Row=D, DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence-tagged connectors: A sequence approach to mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
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                                                                                                                                                                                                                                                                                                                                                                              Length 458;
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                                                                                                                                                                                                                                                                                                                                                                                    Score 48.2; DB 10;
Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 196;
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AQ738512.1 GI:5516034
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34.0%;
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Matches 101; Conservative
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Best Local 9
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                                                                                                                                            /note="Vector: pBACe3.6; Site_1: ECORI; Site_2: ECORI; Male blood DNA was isolated from one randomly chosen donor and partially dispested with a combination of ECORI and ECORI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at ECORI sites"

99 c 369 g 134 t 156 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The library was constructed by Dr. Doug Jasmer (d)asmer@vetmed.wsu.edu) at Washington State University, Dept. of Veterinary Microbiology and Pathology DNA Sequencing by: Washington University Genome Sequencing Center St. Louis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BG520030 466 bp mRNA linear EST 10-MAY-ps29b11.y2 Trichinella spiralis ML CMVsport jasmer Trichinella spiralis cDNA 5' similar to contains element MSR1 repetitive
                                                                                                                                                                                                                                                                                                                                                                                                                      84 gtgggaagggtctgggcaggacctgggctgggctgggtctccttggccctgctgtgtg 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144 tttgcggcaatgctgggtgctgtgactctcggataacctggagatccctgcttttgggcg 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
Contact: McCarter Jp
The Washington Univ. Nematode EST Project, 1999
Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, Pax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nematoda; Enoplea; Trichocephalida;
Trichinellidae; Trichinella.
                                                                      /db_xref="taxon:9606"
/clone="Plate=957 Col=21 Row=D"
/clone_lib="RPCI-11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                      DB 12; Length 843;
                                                                                                                                                                                                                                                                                                                  Score 48; DB 12; Length 84
Pred. No. 1.4;
0; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Washington Univ. Nematode EST Project, 1999
                                                      /organism-"Homo sapiens"
High quality sequence stop: 843.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 element ;, mRNA sequence.
BG520030
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                                                                                                                                                                                                                                                                                                                13.0%;
39.8%;
                                                                                                                                /sex="male"
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                                                                                                                                                                                                                                                                                                                                                   Conservative
                                       .843
                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                 90;
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BG520030/c
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/note="Near-univo"
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Elekaryota; mixed EST libraries.

1 (bases 1 to 937)
Asiegbu.F.O., Nahalkova,J., Choi,W., Stenlid,J. and Dean,R.A.
Expressed sequence tags of randomly selected cDNA clones from the interaction of the root rot fungus (Heterobasidion annosum) with seedling roots of Scots pine (Pinus sylvestris)
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Dept. of Forest Mycology & Pathology
Swedish University of Agriculture, Box 7026,S-750 07, Uppsala,
Sweden
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/clone_lib="Trichinella spiralis
/dev_stage="muscle stage larvae"
/lab_host="DH10B"
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Drosophila melanogaster genome survey sequence T7 end of BAC:
BACR32M17 of RPCI-98 library from Drosophila melanogaster (fruit
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Determination of this BAC-end sequence was carried out as part of a Determination of this BAC-end sequence was carried out as part of a Determination of this BAC-end sequence project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutcoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of
                                                                                                                                                                                                                                                                      /clone_lib="Meterobasidion annosum - Scots pine infection stage subtraction cDNA library (hasp)"
/dev stage="Seedling roots of scots pine were infected for days with H. annosum"
/note="Vector: pT-Adv; Site_l: EcoRI; The subtractive hybridization cDNA library was constructed from scots hybridization cDNA library was constructed from scots pine roots infected for 6-days with mycelia of Heterobasidon annosum (FP5):

a 45 c 767 g 21 t 2 others
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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                                                                                                                                                  1.937
/organism="Pinus sylvestris/Heterobasidion annosum"
/db_xref="taxon:169015"
/clone="hasp001xa23f"
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0; Mismatches 152;
Tel: +46 18 67 15 98
Fax: +46 18 30 92 45
Email: Fred.Asiegpu@mykopat.slu.se
Seq primer: T? primer:
Location/Qualifiers
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of Pichia farinosa, genomic survey sequence.
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Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of brosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
Souciet, J.L., Aigle, M., Artiguenave, F., Casaregola, S.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
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1 (bases 1 to 922)

4 (bancigny, J., Spehner, C., Souciet, J., Tekaia, F., Dujon, B., Wincker, P., Artiquenave, F. and Potier, S. Genomic exploration of the hemiascomycetous yeasts: 15. Pichia
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR32M17"
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11 Similarity 43.4%; Pred. No. 1.7;
82; Conservative 25; Mismatches 82;
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FEBS Lett. 487 (1), 87-90 (2000)
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AL418302.1 GI:12200883
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Genoscope.
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Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: Sacquelgenoscope.cns.fr. web: www.genoscope.cns.fr.)
This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces actions var. uvarum, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces hluyveromyces thermotocherans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Sacharomyces hansenii var. hansenii, Pichia sorbitophila, S kb were prepared and both extremities were sequenced See keywords for description of this sequence and for the sequence of the other extremity of this insert.

Location/Qualifiers
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12.9%; Score 47.6; DB 12; Length
Best Local Similarity 42.4%; Pred. No. 1.7;
Matches 104; Conservative 14; Mismatches 127; Indels
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/organism="Pichia farinosa"
/strain="c88 7064"
/db_xref="taxon:4920"
/clone="AXOAA030F01"
/clone=lib="AXOAA"
/note="end : T7"
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Job time: 7529 sec
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CUMPUTER NELLANDER COMPUTER IN TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible OPERATING SYSTEM: PG-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CUSPTWARE: Patentin Release #1.0, Version #1.25 CUSPTWARE: Patentin Bath Release #1.0, Version #1.25 CUSPTWARE: Patentin DaTA: APPLICATION NUMBER: US/09/935,313 FILING DATE: APPLICATION NUMBER: US/07/935,313 FILING DATE: APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: APPLICATION NUMBER: S.6+01991 ATTORNEY/GENT INFORMATION: REFERENCE/DOCKET NUMBER: 30472/114 IMMU TELECOMMUNICATION INFORMATION: TELEPHONE: (703)683-4109 TELECAMMUNICATION INFORMATION: TELEPAX: (703)683-4109 TELECAM: APPLICATION TOPOLOGY: APPLICATION TOPOLOGY: Linear IMMEDIATE SOURCE: CLONE: ALIGABLE SOURCE: CLONE: PIZGPL-FIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14, Application US/08232463
Fatent No. 5670367
GENERAL INFORMATION:
APPLICANT: SCHEFFLINGER, F.
APPLICANT: SCHEFFLINGER, F.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-232-463-14/C
                                                                                                                          May 24, 2002, 00:20:45; Search time 121.39 Seconds (without alignments) 748.698 Million cell updates/sec
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Sequence 12, Appl
Sequence 13, Appl
Sequence 14, Appl
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Sequence 8, Appli
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370
1 tgcgattgcccagcaaatgc.....atgaggacgcctgccggcc 370
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. /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

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! /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

! /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

! /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

! /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
     14.5
Compugen Ltd.
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US-09-165-264-12
US-09-165-264-13
US-09-165-264-14
US-09-165-264-14
US-09-165-264-7
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US-08-370-156-26
US-08-318-826A-5
US-08-370-156-1
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US-07-793-961A-1
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GenCore version
Copyright (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries
                                                                                    · nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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53577
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	ALIGNMENTS					
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Sequence 4, Appl1	US-08-282-696-4	7 (	1000	, o	32.0	* 5
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-	US-08-459-586-4	-	18994	8.0	33	43
-	US-07-945-283-1	-	8438	8 6.8	33	42
6	US-08-282-696-9	~	1702	6.8	33	1.4
. 6	US-08-459-586-9	-	1702	6.8	33	40
ì =	US-08-458-568A-11 .	-	12001	9.0	33.4	39
-	US-09-130-032A-1	N	4425	9.0	33.4	ი 38
-	US-08-749-169A-1	~	4425	9.0	33.4	c 37
Sequence 1, Applit	US-08-843-659-1	4	4257	0.6	33.4	c 36
- i	US-09-259-821A-1	4	4257	9.0	33.4	c 32
_	US-08-690-473-1	7	4257	0.6	33.4	c 34
1	5215881-2	9	2721	0.6	33.4	33
- 1	US-09-499-884-11	4	3663	9.1	33.6	32
ì ,-	US-09-165-543-1	m	2689	9.1	33.8	c 31
_	US-08-985-090-1	~	2689	9.1	33.8	0F 0
	US-08-750-703-4	~	8779	9.2	34	67
Sequence 2. Appl (	US-08-750-703-2	7	1737	9.5	34	28

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                                                                                                  LENGTH: 152331
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                                                                                                                                           FEATURE:
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                                                                         Sequence 16, Application US/09128155
Patent No. 6117654
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: 09404/05201
CURRENT APPLICATION NUMBER: US/09/128,155
                                                                                                                                                                                                           186 gatccctgcttttggggcgaatccggggggtagttgctcatcaagactagaggtggggtgg 245
                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence:Primer sequence US-09-165-264-8
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                                                  ggectgtgggaagggtetgggeetggeaggaectgggetggggteteettggeeet 134
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Length 7218;
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                          Indels
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; Patent No. 6197510
; GENERAL INFORMATION:
   APPLICANT: Vinayagamoorthy, Thuraiayah
   TITLE OF INVENTION: Multi-Loci Genomic Analysis
   FILE REFERENCE: 44747
; CURRENT APPLICATION NUMBER: US/09/165,264
; CURRENT APLICATION DATE: 1998-10-01
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 2.1
 13.6%; Score 50.4; DB 1; Similarity 0.9%; Pred. No. 0.00045; 3; Conservative 214; Mismatches 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 39.2; DB
Pred. No. 0.15;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.6%;
58.6%;
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Matches 68; Conserva
     Query Match
Best Local Similarity
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LENGIH: 319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence:Primer sequence US-09-165-264-12
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 10.2%; Score 37.6; DB 4; Length 318; Best Local Similarity 56.5%; Pred. No. 0.38; Matches 70; Conservative 0; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Vinayagamoorthy, Thuraiayah
TITLE OF INVENTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44747
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEO ID NOS: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22144 GGGCGGGCGGGGGGGGGGCGCTCGCTGCGG 22110
                                                                                                                                                                                                                                                                                                                                                               Score 39; DB 3 Pred. No. 0.62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87 ggaagggtctgggcctggcaggacctgggctgggg 121
                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER FILING DATE: 1997-08-04
NUMBER OF EQ ID NOS: 18
SEQ ID NO 16
SEQ ID NO 16
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US-09-165-264-13
'Sequence 13, Application US/09165264
; Patent No. 6197510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12, Application US/09165264 Patent No. 6197510
                                                                                                                                                                                                                                            // NAME/KEY: misc_feature
// LOCATION: (1)...(152331)
// OTHER INFORMATION: n = A,T,C or G
US-09-128-155-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                   10.5%;
63.2%;
                                                                                                                                                                                                                                                                                                                                                                     Query Match 10.5
Best Local Similarity 63.2
Matches 60; Conservative
                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
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79 ggcctgtgggaagggtctgggcctggacctgggctggggtctccttggcctggtg 138
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10.0%; Score 37; DB 4; Length 320;
Best Local Similarity 47.3%; Pred. No. 0.54;
Matches 112; Conservative 0; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Brake, Anthony J.
APPLICANT: Brake, Anthony J.
APPLICANT: Kaufman, Rnadal J.
APPLICANT: Washey, Louise
APPLICANT: Washey, Louise
TITLE OF INVENTION: Expression of PACE in Host Cells and
TITLE OF INVENTION: Methods of Use Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Howson & Howson
Spring House Corporate Center, P.O. Box 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/885,972A
FILING DATE: 19920520
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/621,092
FILING DATE: 26-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,859
FILING DATE: 29-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-07-885-972A-3/c
; Sequence 3, Application US/07885972A
; Patent No. 5460950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: Spring House Corporate CITY: Spring House CITY: Spring House STATE: Pennsylvania COUWTRY: U.S.A.

ZIP: 19477
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS/MS-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                     19 ရှင်ရှာစရာရှင်ရှင်ရှာရှာရှင်ရှင်ရှင်ရှင်ရှင်ရှင်ရှင်ရေးရှင်ငေရေးရှင်ငင်ရှာရှုရှ်ရှင်ရှာရှုရှိရှင်ရှာရှ 78
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US-09-165-264-14
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Best Local Similarity 59.3%; Pred. No. 0.38;
Matches 64; Conservative 0; Mismatches 44; Indels
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10.1%; Score 37.2; DB 4; Length 320;
Best Local Similarity 56.6%; Pred. No. 0.48;
Matches 69; Conservative 0; Mismatches 53; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Vinayagamoorthy, Thuraiayah
TITLE OF INVENTION: Multi-Loci Genomic Analysis;
FILE REPERENCE: 44747
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILLING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 13
LENGTH: 320
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/09165264

Fatent No. 6197510

GENERAL INFORMATION:
APPLICATIVE OF INVENTION: Multi-Loci Genomic Analysis
FILE REPRENCE: 44747

CURRENT APPLICATION NUMBER: US/09/165,264

CURRENT FILING DATE: 1998-10-01

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 14

LENGTH: 320
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Sequence 7, Application US/09165264

Patent No. 6197510

; GENERAL INFORMATION:
                                                                                                                                                                          ORGANISM: Artificial Sequence
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JMBER: US 07/621,092
26-NOV-1990
FILING DATE: 20-MAY
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
LOCATION:
US-08-745-880-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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Pred. No. 1.7;
0; Mismatches 40; Indels
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APPLICANT: Wordy, Polly A
TITLE OF INVENTION: Expression of PACE in Host Cells and
TITLE OF INVENTION: Methods of Use Thereof
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson & Howson & Howson STREET: Spring House Corporate Center, P.O. Box 457
CITY: Spring House
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC COMPATIBLE
SOFTWARE: PatentIn Release #1.0, Version #1.25
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APPLICATION NUMBER: US 07/621,443
FILING DATE: 29-00v-1990
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/621,457
FILING DATE: 30-00v-1990
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REGISTRATION NUMBER: 31515
RECISTRATION NUMBER: GI5181A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
INFORMATION FSEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH 4465 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
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APPLICATION NUMBER: US 08/480,382
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 07/885,972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/745,880 FILING DATE: 08-NOV-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Barr, Philip J.
APPLICANT: Brade, Anthony J.
APPLICANT: Kaufman, Rnadal J.
APPLICANT: Tekamp-Olson, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/08745880 Patent No. 5965425
                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 60.0%;
Matches 60; Conservative
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U.S.A.
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408..2789
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                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
COCATION:
US-07-885-972A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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Gaps
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Sequence 3, Application US/08480382

Patent No. 5986079

GENERAL INFORMATION:
APPLICANT: Barr, Pathip J.
APPLICANT: Reafman, Rnadal J.
APPLICANT: Reafmap-Olson, Patricia
APPLICANT: Wasley, Louise
APPLICANT: Wong, Polly A.
TITLE OF INVENTION: Expression of PACE in Host Cells and
TITLE OF INVENTION: Methods of Use Thereof
NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 4405;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DAR: US/NR///
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pred. No. 1.7;
0; Mismatches
FILING DATE: 26-NOV-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,859

FILING DATE: 29-NOV-1990

PRIOR APPLICATION NUMBER: US 07/621,443

APPLICATION NUMBER: US 07/621,443

FILING DATE: 29-NOV-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/621,457

ATPLICATION NUMBER: US 07/621,457

ATTING DATE: 30-NOV-1990

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Bak, Mary E. REGISTRATION NUMBER: 31,215
REGISTRATION NUMBER: G15181A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-2206
TELEPRAX: 215-540-5818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Howson & Howson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 9.7%;
Best Local Similarity 60.0%;
Matches 60; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4405 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
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408..2789
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; OTHER INFORMATION: Description of Artificial Sequence:Primer sequence US-09-165-264-11
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Sequence 11, Application US/09165264
Sequence 11, Application US/09165264
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
MILI-LEREPRENCE: 44747
CURRENT FAPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
SOFTWARE: Patentin Ver. 2.1
SEQ 1D NO 11
LENGTH: 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.7%; Score 35.8; DB 4;
51.1%; Pred. No. 1.9;
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9.7%; Score 35.8; DE
Best Local Similarity 61.1%; Pred. No. 1.9;
Matches 58; Conservative 0; Mismatches
                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/243,391
FILING DATE: 13-MAY-1994
PRIOR APPLICATION NUMBER: US 07/985,586
FILING DATE: 03-DEC-1992
PRIOR APPLICATION NUMBER: US 07/985,586
FILING DATE: 03-DEC-1992
PRIOR APPLICATION NUMBER: US 07/91,533
FILING DATE: 10-JUL-1992
PRIOR APPLICATION NUMBER: US 07/787,840
FILING DATE: 05-NOV-1991
PRIOR APPLICATION NUMBER: US 07/789,188
FILING DATE: 05-NOV-1991
PRIOR APPLICATION NUMBER: DCT/US93/11704
FILING DATE: 05-DEC-1993
PRIOR APPLICATION NUMBER: PCT/US93/11704
FILING DATE: 02-DEC-1993
PRIOR APPLICATION NUMBER: PCT/US93/11704
FILING DATE: 05-NOV-1991
APPLICATION NUMBER: PCT/US93/11704
FILING DATE: 05-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: VACUATION NUMBER: PCT/US92/09627
ATTORNEY/AGENT INFORMATION:
                           MBER: US/08/406,030A
17-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Granhan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: TKT9:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-406-030A-3
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ORGANISM: Artificial Sequence
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 36; DB 2; Length 4405;
Pred. No. 1.7;
0; Mismatches 40; Indels
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APPLICANT: Heartlein, Michael W.
APPLICANT: Heartlein, Michael W.
APPLICANT: Selden, Richard F
TTTLE OF INVENTION: Protein Production and Delivery
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: TWO Militia Drive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 ggcctgtgggaagggtctgggcctggcaggacctgggctg 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 26-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,859
FILING DATE: 29-NOV-1990
PRIOR APPLICATION NUMBER: US 07/621,443
FILING DATE: 29-NOV-1990
PRIOR APPLICATION NUMBER: US 07/621,457
FILING DATE: 39-NOV-1990
APPLICATION NUMBER: US 07/621,457
FILING DATE: 30-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E: REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: 31,215
REFERENCE/DOCKET NUMBER: GISIBIA
TELECOMMUNICATION INFORMATION:
TELEPRAX: 215-540-2206
TELEFRAX: 215-540-5818
SEQUENCE CARRACTERS:
SEQUENCE CHARACTERS:
LENGTH: 4405 base pairs
"VEFF: NUMBER: GISIBIA TELEFRAX: 215-540-5818
FILING DAIL.

CLASSIERCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/885,972
FILING DATE: 20-MY-1992
APPLICATION NUMBER: US 07/621,092
APPLICATION NUMBER: US 07/621,092
APPLICATION NUMBER: US 07/621,092
APPLICATION NUMBER: US 07/621,092
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 60.0%;
Matches 60; Conservative
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EDNESS: double
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STATE: Massachusetts
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US-08-480-382-3
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TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-07-793-961A-1
STRANDEDNESS:
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                                                                                                                                                                                                  Gaps
                                                                                                                                 .;
                                     Length 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Yoshihiro Ishikawa
TITLE OF INVENTION: Cloning and Character-
TITLE OF INVENTION: ization of a Cardiac Adenylyl Cyclase
                                  9.6%; Score 35.6; DB 4; Length 3 ilarity 44.6%; Pred. No. 1.2; Conservative 0; Mismatches 174; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Alan M. Gordon
ADDRESSEE: American Cyanamid Company
SPREET: 1937 West Main Street,
STREET: P.O. Box 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/07/793,961A
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SEQUENCE CHARACTERISTICS:
LENGTH: 4046 base pairs listed
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/07793961A Patent No. 5334521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Gordon, Alan M.
REGISTRATION NUMBER: 30,637
REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203 321 2719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: MS-DOS SOFTWARE: ASCII from DW4 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07 FILING DATE: 19911118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                  319 tcactccgcagaaa 332
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STATE: Connecticut
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APPLICANT: YOShih
                                                        Local Similarity
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US-07-793-961A-1
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                                                           Best Local Sim
Matches 140;
                                          Query Match
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    Length 4046;
                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ishikawa, Yoshihiro
TITLE OF INVENTION: Cloning and Characterization of a
TITLE OF INVENTION: Cardiac Adenylyl Cyclase
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TIFE: FIGHT COMPATIBLE
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/240,357
FILING DATE: 10-MAY-1994
CLLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GOLDON, Alan M.
REFERENCE/DOCKET NUMBER: 30,637
REFERENCE/DOCKET NUMBER: 31,705-01
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                36;
    DB 1;
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); Mismatches
Score 35.4; D. Pred. No. 2.3;
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                                                                                                0; Mismatches
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STREET: One Cyanamid Plaza
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TELEFAX: 201-831-3305
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
Query Match 9.6%;
Best Local Similarity 61.3%;
Matches 57; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
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Best Local Similarity 61.3
Matches 57; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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STATE: New Jersey
COUNTRY: USA
ZIP: 07470-8426
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; LOCATION:
US-08-240-357-1
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RESULT 15
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Search completed: May 24, 2002, 00:21:22 Job time: 11748 sec

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Primer used in the
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                    polynucleot1
                                colon cancer
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Human immune/haema
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trinucleotide repeat protein; TRP; T243; embryonic stem cell; ES; transgenic animal; knockout mouse; triplet repeat expansion; fragile X syndrome; Huntington's disease; mouse; ds.
         Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7243 gene homologous sequence #2 generated by PCR.
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AAC90316
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   AAS05285 standard; DNA; 370
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10468
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WO200130798-A1.
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1208.635 Million cell updates/sec
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Human gene express
Human cacng&L cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                     1: /SIDS1/gogdata/geneseqn.embl/NA1980.DAT;*
2: /SIDS1/gogdata/geneseqn.embl/NA1981.DAT;*
3: /SIDS1/gogdata/geneseqn.embl/NA1981.DAT;*
4: /SIDS1/gogdata/geneseqn.embl/NA1981.DAT;*
5: /SIDS1/gogdata/geneseqn.embl/NA1981.DAT;*
6: /SIDS1/gogdata/geneseqn.embl/NA1981.DAT;*
7: /SIDS1/gogdata/geneseqn.embl/NA1981.DAT;*
7: /SIDS1/gogdata/geneseqn.embl/NA1980.DAT;*
8: /SIDS1/gogdata/geneseqn.embl/NA1980.DAT;*
8: /SIDS1/gogdata/geneseqn.embl/NA1980.DAT;*
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8: /SIDS1/gogdata/geneseqn.embl/NA1992.DAT;*
8: /SIDS1/gogdata/geneseqn.embl/NA1999.DAT;*
8: /SIDS1/gogdata/geneseqn.embl/NA20018.DAT;*
                                                                                                                     US-09-696-686-51
370
1 tgcgattgcccagcaaatgc.....atgaggacgcctgccggcc 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                      May 24, 2002, 00:24:32; Search time 525.6 Seconds
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                             lotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                        1736436 segs, 858457221 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                             · nucleic search, using sw model
                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAL05795
AAZ17263
AAF81304
AAS80100
AAZ32028
AAC90085
AAX53491
AAX02974
                                                                                                                                                                     IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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4362
1337
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114955
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Match
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111.3
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113...
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Result š.

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2000US-0231968
2000US-0232397
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2000US-0198123
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cancer; gene therapy;
                                                         WO200155320-A2
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                                                                                                                                                                                                                                                19-MAY-2000;
                                Homo sapiens
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                                                                                      02-AUG-2001
   The present sequence for T243 homologous sequence #2 is generated by PCR and is homologous to the T243 gene which encodes for a trinucleotide repeat protein (TRP). The invention describes methods of producing embryonic stem (ES) cells comprising a heterozygous disruption in a gene comprising a heterozygous disruption in a gene producing a knockout mouse comprising a homozygous disruption in a gene concoding TRP, where the disruption inhibits the production of the wild encoding TRP. The invention also relates to identifying agents capable of affecting a phenotype of a knockout mouse. Also described are methods of determining whether expansion of the trinucleotide repeat in a gene concoding TRP produces a phenotypic change. The transgenic animals and the concoling TRP produces a phenotypic change. The transgenic animals and the concoling TRP produces a phenotypic change. The transgenic animals and the calls are useful for identifying compounds capable of ameliorating cells are useful for identifying compounds capable of ameliorating disease symptoms, and as test substrates for the identification of drugs, treating trinucleotide repeat disorders e.g. fragile X syndrome and treating trinucleotide repeat disorders e.g. fragile X syndrome and ciscaders are ideal model systems to study the progression of disease in ciscaders are ideal model systems to study the progression of disease in convivo, the molecular basis of these diseases and show the features observed in human disease. Using the mice, it is possible to model both
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; reproductive system related antigen; reproductive system disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Length 370;
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         contains heterozygous disruption in a gene encoding IRP
                                                                                                                                                                                                                                                                                                                                                                                     62 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 370; DB 22;
100.0%; Pred. No. 5.4e-87;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 370 BP; 73 A; 86 C; 149 G;
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1D AAL05795 standard; DNA; 4362 BP.
XX
AC AAL05795;
XX
DT 21-NOV-2001 (first entry)
XX
XX
XX
KW
Human reproductive system related
XX
KW
Human; reproductive system related
                                       Claim 11; Fig 14; 106pp; English.
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Matches 370; Conservative
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2000US-0241826
2000US-0246474
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2000US-0241786.
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2000US-0249211.
2000US-0249212.
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20000S-0249264.
20000S-0249265.
20000S-0249265.
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2000US-0236368
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2000US-0236802
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2000US-0241221.
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2000US-0251990.
2000US-0254097.
2001US-0259678.
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2000US-0249300
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2000US-0251856
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25-SEP-2000;
27-SEP-2000;
27-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
20-CCT-2000;
02-CCT-2000;
03-CCT-2000;
03-CCT-2000;
03-CCT-2000;
04-CCT-2000;
06-CCT-2000;
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08-NOV-2000;
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06-DEC-2000;
08-DEC-2000;
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17-NOV-2000;
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17-NOV-2000;
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05-DEC-2000;
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05-JAN-2001;
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                                                                                                                                                          The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                      3725 GCGCGCCGCTGGGCCGGGGCCAAGGCCTCGCAGGAGGAGGAGGAGGACCAAGGG 3666
                                                                                         Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition .
                                                                                                                                                                                                                                                                                                                                                                                        71 gggggcgggggcctgtgggaagggtctgggcctggcaggacctgggctggggtctccttgg 130
                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                     Human; gene; gene expression product; diagnosis; therapy; probe;
detection; mapping; tissue typing; profiling; forensic; cancer;
genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
                                                                                                                               Disclosure; SEQ ID NO 8483; 1297pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                      Length 4362;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Crkvenjakov R, Dickson M, Drmanac R, Drmanac S;
Escobedo J, Garcia PD, Garcia V, Giese K, Innis MA;
Jones WL, Kassam A, Kennedy GC, Kita D, Labat I;
Lamson G, Leshkowitz D, Pot D, Randazzo F, Reinhard C;
                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                      Sequence 4362 BP; 978 A; 1225 C; 1182 G; 977 T; 0 other;
                                                                                                                                                                                                                                                                                  11.5%; Score 42.4; DB 22;
58.9%; Pred. No. 0.15;
tive 0; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP.
                                         Ruben SM;
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ID AAZ17263 standard; cDNA; 1337
            (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0080666.
98US-0072910.
98US-0075954.
98US-0080114.
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                                                                                                                                                                                                                                                                                                             73; Conservative
                                         Barash SC,
                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                 WPI; 2001-465570/50
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24-FEB-1998;
31-MAR-1998;
03-APR-1998;
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                                       Rosen CA,
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25-SEP-2000; 2000WO-GB03685.

WO200121791-A2

29-MAR-2001

99GB-0022571

23-SEP-1999;

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The present invention describes a library of human polynucleotides

comprising the sequences given in AA212532 to AA21779. Also described is

comprising the sequences given in AA212532 to AA217779. Also described is

can method of detecting differentially expressed genes correlated with the

can cancerous state of a mammalian cell, comprising detecting at least one

differentially expressed gene product in a test sample from a cell

can ferentially expressed gene product in a test sample from a cell

confirmed for a variety of purpose, e.g. detection of expression levels,

con be used for a variety of purpose, e.g. detection of expression levels,

can be used for raising artibodies for experimental, diagnostic and

can be used for raising artibodies for experimental, diagnostic and

charapeutic purposes. The polynucleotides may also be used to construct

carrays for diagnostics (which may be used to determine function of an

concerls (e.g. to identify abnormal or diseased tissue in a human, to

two cells (e.g. to identify abnormal or diseased tissue in a human, to

concerly prognosis and management of colorectal cancer, breast cancer,

diagnosis, prognosis and management of colorectal cancer, breast cancer,

and lung cancer. The polynucleotides can also be used to screen for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; stargazin-like; CACNGBL; anticonvulsant; hypotensive; vasotropic; antiarrhythmic; antianginal; analgesic; nootropic; cytostatic; neuroprotective; cerebroprotective; antidiabetic; antimigraine; antiarteriosclerotic; immunosuppressive; antiparkinsonian; auditory; ophthalmological; tranquiliser; neuronal disorder; calcium channel modulation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ggcctgtgggaagggtctgggcctggcaggacctgggctggggtctccttggccctgctg 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tgtgctttgcggcaatgctgggtgctgtgactctcggataacctggagatccctgctttt 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                  Novel human genes and their expression products which are differentially expressed in different cell types
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1337 BP; 42 A; 577 C; 27 G; 22 T; 669 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 41.8; DB 20;
Pred. No. 0.16;
0; Mismatches 144;
Williams LT;
                                                                                                                             Claim 1; Page 2250-2251; 2479pp; English.
 Sudduth-Klinger J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide analogues and antagonists.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 11.3%;
Best Local Similarity 38.7%;
Matches 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                     WPI; 1999-494092/41.
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   Stache-Crain B,
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Homo sapiens

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The present sequence is provided in a specification relating to an isolated stargazin-like polypeptide comprising a sequence of 327 or 275 scaled a city of modulating the steady state. The polypeptide is useful for treating a muino acids fully defined in the specification, or its variant capable of modulating the steady state. The polypeptide is useful for treating a subject having a neuronal disorder that is responsive to calcium channel modulation. It is useful in the manufacture of a medicament for treatment or prophylaxis of a disorder that is responsive to calcium channel modulation, e.g. epilepsy, episodic ataxia, spinocerbellar ataxia, hypertension, ischaemic heart disease, neuroprotection, stroke, pain, cerebral ischaemic hadrensclerosis, tardive dyskinesias, peripheral vascapasm, atherosclerosis, tardive dyskinesias, nigraine, hadache, bipolar disorders, unipolar depression, anxiety, parkinson's disease, cognitive disorders, ophthalmic diseases, neuromuscular disorders and tinnitus. Nucleic acids encoding these polypeptides are useful in the production of the polypeptides, and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel stargazin-like polypeptides capable of modulating the steady state inactivation of an alphal pore-forming subunit of a voltage-gated calcium channel, for treating central nervous system disorders
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Pred. No. 0.22;
0; Mismatches 113;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAS80100 standard; cDNA; 972
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Best Local Similarity 49.1%;
Matches 109; Conservative
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                                                                                                                                                                                                                                                                                                                 (GLAX ) GLAXO GROUP LTD.
                                                                                                                                                                                                                                                                                                                                                                                        Plumpton M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001-266074/27.
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P-PSDB; AAB73982
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us-09-696-686-51.rng

AAZ32028 standard; DNA; 38186 BP.

AAZ32028

(first entry)

10-JAN-2000

AAZ32028;

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags (or identifying expressed genes. (I) is useful in gene therapy techniques (I restore normal activity of (II) or to treat disease states involving (II). (II) and its binding antibodies against it, detecting or a food supplement. (II) and its binding partners are useful in medical mading of sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. (The polypeptide and polymorleotide sequences have applications in caponsible for genetic disorders or other traits to assess biodiversity conditional and products dependent on DNA and conditional and products dependent on DNA and conditional and products dependent on DNA and diagnostics, formations for the produce other types of data and products dependent on DNA and continuous of the produce other types of the product of produce other types of the products dependent on DNA and diagnostics formations for the products dependent on DNA and diagnostics formations for the products dependent on DNA and diagnostics formations for the products dependent on DNA and diagnostics formations for the products dependent on DNA and diagnostics formations for the products dependent on DNA and diagnostics formations for the products dependent on DNA and diagnostics formations for the products dependent on DNA and diagnostics formations for the products dependent on DNA and diagnostics formations for the products dependent on DNA and diagnostics formations for the products dependent on DNA and diagnostics formations for the products dependent on DNA and diagnostics formatics formations for the products dependent on DNA and diagnostics formations for the products dependent on DNA and diagnostics
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                  Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, useful in dlagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess blodiversity .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID No 15904; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tang YT;
                                                                                                                                                                                                                                                                                                                                                          31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                    30-MAR-2001; 2001WO-US08631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC
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                                                                                                                                                                                 WO200175067-A2.
                                                                                                                        Homo sapiens.
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                                                                                                                                                                                        105 gggagcgtggcgactagttgcacagcaacggtccaggaagatgagtgcctgcgggaggaa 164
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                                                                                   Gaps
                                                                                                                                                                                                                                                 165 ggccctgaccctgctgagcagtgtctttgctgtctgtgggcttgggcctcctgggtatcgc 224
                                                                                                    DB 23; Length 972;
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Sequence 972 BP; 193 A; 291 C; 266 G; 222 T; 0 other;
                                                                                                                                                                                                                                                                                9989atccctgcttttgggcgaatccgggggtagttgctcat 224
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                                                                           0; Mismatches 113;
                                                 Score 41.2; DB
Pred. No. 0.22;
                                              11.18;
                                         Ouery Match
Best Local Similarity 49.1
Matches 109; Conservative
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AA232000 and AA232001 encode, and AAY49501 and AAY49502 represent, human metalloprotease thrombospondin (METH) proteins METH1 and METH2

respectively. METH1 and METH2 have been found to be potent inhibitors of angiogenesis both in vitro and in vivo. They can be used for treating cancer and other disorders related to angiogenesis including abnormal wound healing, inflammation, rheumatoid arthritis, psoriasis, endometrial bleeding disorders, diabetic retinopathy, some forms of macula degeneration, hemanajomas, and arterial venous malformations. They may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the proliferation, differentiation, or mobilisation (chemotaxis) of immune cells. The etiology of these immune deficiencies or disorders may be genetic, somatic, such as cancer or some autoinmune disorders, acquired (e.g. by chemotherapy or toxins), or infectious. They can also be used to treat inflammatory cused for detection and diagnosis. AA232002 to AAX32080, and AAX49503 to harvein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated metalloprotease thrombospondin polypeptides, useful for treating hyperproliferative disorders, cancers or autoimmune disorders
                                                                                                     Human; METH1; METH2; anti-anglogenic; metalloprotesse thrombospondin; cancer; diagnosis; hyperproliferative disorder; autoimmune disease, anglogenesia inhibitor; abnormal wound healing; inflammation; rheumatoid arthritis; psoriasis; endometrial bleeding disorder; diabetic retinopathy; macula degeneration; haemangloma; detection; arterial venous malformation; immune deficiency; ss.
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Pred. No. 1.1;
0; Mismatches 60; Indels
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                                                                       Human METH1 related EST AC004449.
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                                                                                                                                                                                                                                                                                                                                                                         98US-0072298.
98US-0098539.
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                                                                                                                                                                                                                                                                                                                                                                                                                            (IRUE/) IRUELA-ARISPE L. (HAST/) HASTINGS G A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 55.9
Matches 76; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               RUBE/) RUBEN S M.
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                                                                                                                                                                                                                                  Homo sapiens.
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28-AUG-1998;
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                                                                                                                                                                                                            METH; metalloprotease; thrombospondin; angiogenesis inhibition; cancer therapy; benign tumour; ocular angiogenic disease; rheumatoid arthritis; psoriasis; wound healing; endometriosis; vasculogenesis; granulation; hypertrophic scar; nonunion fracture; scleroderma, trachoma; vascular adhesion; myocardial angiogenesis; ocronary collateral; cerebral collateral; arteriovenous malformation; ischaemic limb angiogenesis; osler-webber syndrome; wound granulation; plaque neovascularisation; telangiectasia; haemophiliac joint; EST; angiofibroma; fibromuscular dysplasia; expressed sequence tag; Crohn's disease; atherosclerosis; birth control; ss.
                       METH1 and METH2 polynucleotides and encoded polypeptides, used to inhibit angiogensis in the treatment of disorders such as cancer, rheumatoid arthritis and psoriasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trulli SH;
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BETH ISRAEL DEACONESS MEDICAL CENT.
IRUELA-ARISPE L.
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                                                                                                                                 BP.
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Fornwald JA, Terrett JA;
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20-JUL-1999; 99US-0144882.
10-AUG-1999; 99US-017823.
13-AUG-1999; 99US-0373658.
22-DEC-1999; 99US-0171503.
22-FEB-2000; 2000US-0183792.
                                                                                                                                 AAC90085 standard; DNA; 38186
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                                                                             2819 acgctggccaaggtgc 2834
                                                                                                                                                                            (first entry)
                                                          128 tggccctgctgtgtgc 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TRUL/) TRULLI S H.
(FORN/) FORNWALD J A.
(TERR/) TERRETT J A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HASTINGS G A.
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                                                                                                                                                                                               AC004449 cDNA clone
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JONAK Z L.
                                                                                                                                                                                                                                                                                                                                                       WO200071577-A1.
                                                                                                                                                                                                                                                                                                                                     Unidentified.
                                                                                                                                                                           19-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                            30-NOV-2000
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(HAST/)
(RUBE/)
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                 68
                                                                                                                        AAC90085
                                                                                                               RESULT
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rheumatoid arthritis, psoriasis, delayed wound healing, endometriosis, vasculogenesis, granulations, hypertrophic scars, nonunion fractures, scleroderma, trachoma, vascular adhesions, myocardial angiogenesis, coronary collaterals, cerebral collaterals, arteriovenous malformations, ischaemic limb anglogenesis, Osler-Webber syndrome, plaque neovascularisation, telangiectasis, haemophilae joints, angiofibroma, fibromuscular dysplasia, wound granulation, Crohn's disease or atherosclerosis. METH can also be used in diagnostic methods for the prognosis of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antisense oligonucleotide; multiple target; antisense treatment; impaired respiration; inflammation; lung disease; pulmonary vasoconstriction; inflammation; allergic rhinitis; acute asthma: allergy; asthma: impeded respiration; respiratory distress syndrome; pain; cystic fibrosis; pulmonary basoconstriction; emphysema; pulmonary basoconstriction; emphysema; chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma; hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antisense oligonucleotides used in treatment of, e.g. pulmonary vasoconstriction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human adenosine Al receptor antisense oligonucleotide fragment.
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                                                                                                                                                                                                                                                                                                                                                                        10.8%; Score 40; DB 22; Length 38186; 55.9%; Pred. No. 1.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2819 acgctggccaaggtgc 2834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 tggccctgctgtgtgc 143
                                                                                                                                                                                                                                                                                                                                                                                       Query Match 10.89
Best Local Similarity 55.99
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prostate cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-229400/19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-JUN-1998;
17-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAX53491;
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The specification describes antisense oligonucleotides (AAX52869-X55271)

directed against at least 2 mRNAs selected from target genes, coding and
non-coding regions of RNAs corresponding to target genes, gene
initiation codons, genomic flanking regions, intron-exon borders, the
confine and all segments of RNAs encoding proteins associated with one
confine and all segments of RNAs encoding proteins associated with one
confine and all segments of RNAs encoding proteins associated with one
confine and all segments of mixtures. The antisense oligonucleotides
confidenced from sequences AAX55180-271) can be used for the
antisense treatment of diseases and conditions. Typical diseases and
conditions are those associated with impaired respiration and
conditions are those associated with impaired respiration and
inflammation, including lung diseases, pulmonary vasoconstriction,
conditions, respiratory distress syndrome, pain, cystic fibrosis,
crespiration, respiratory distress syndrome, pain, cystic fibrosis,
crespiration, respiratory distress syndrome, pain, cystic fibrosis,
conditions are concernomes of conditions, indicated cancer, lung cancer,
conditions are cancer, hepatocellular carcinoma, kidney cancer, melanoma,
conditions are distress, as well as all types of cancers which may metastasize
conditions the distress and conditions and prostate cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 108020 gcgcctggctcgcctbgggccccsnnndnnggcgggggggggggggcggctggctcgcctbg 108079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 108140 gcggcgcctggctcgcctbgggcsnnndnnggcgggggggggggcgcctggctcgcc 108199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 108200 tbgggsnnndnnggcgggggggggggggcgcctggctcgcctbggsnnndnnggcggggggg 108259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tango-77; human; IL-1ra; cytokine superfamily; inflammation; inhibition; interleukin-1 receptor; IL-1R; regulation; asthma; rheumatoid arthritis; chronic myelogenous leukaemia; psoriasis; inflammatory bowel disease; growth factors; treatment; IL-1 receptor complex; BAC; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 ggggcgggaggggggggcctgtgggaagggtctgggcctggcaggacctggggctgggg 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 114955 BP; 6071 A; 29417 C; 36712 G; 21328 T; 21427 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 gcgattgcccagcaaatgcgaaggtgagggggggggcgcgcgggggcgtagccaagcccga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 tctccttggccctgctgtgtgctttgcggcaatgctgggtgctgtgactctcggataacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 tggagatccctgcttttgggcgaatccgggggtagttgctcatcaagactagaggtggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 114955;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human IL-1ra BAC contiguous DNA sequence 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.7%; Score 39.6; D. 39.4%; Pred. No. 1.7;
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ID AAX02974 standard; DNA; 3198 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 10.7%;
Best Local Similarity 39.4%;
Matches 97; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9906426-A1
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AAX02956-X03048 and AAX22301-X22304 are overlapping BAC genomic sequences containing alternatively spliced forms of human IL-Ira. Such fragments are used in the method of the invention which describes the isolation of a novel human TANGO-77 encoding nucleic acid and protein. Tango-77 is a member of the cytokine superfamily that is expected to Thibit inflammation by binding to the interleukin-1 receptor (IL-IR). It processes associated with acute or chronic inflammation, e.g. asthma, chronic myelogenous leukaemia, rheumatoid arthritis, psoriasis and inflammatory bowel disease. It may also induce or suppress interleukins, cytokines and growth factors. Modulators of this protein are used to treat or prevent conditions associated with abnormal levels of inflammation, or activity of IL-1 or its receptor complex.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; reproductive system related antigen; reproductive system disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid encoding the new human cytokine Tango-77 used to inhibit inflammation and to screen for specific modulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human reproductive system related antigen DNA SEQ ID NO: 9859.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           35; Indels
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3198 BP; 807 A; 847 C; 681 G; 846 T; 17 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87 ggaagggtctgggcctggcaggacctgggctgggg 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                            (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
                                                                                                                                                       Example 5; Figure 3; 226pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                               th 10.5%;
1 Similarity 63.2%;
60; Conservative
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2000US-0189874.
2000US-0190076.
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2000US-0205515.
2000US-0209467.
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2000US-0184664
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                                                                                  WPI; 1999-153692/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 60; Conserv
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04-AUG-1997;
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19-MAY-2000;
07-JUN-2000;
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                                                       Pan Y;
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28-JUN-2000; 2000US-0214886.
30-JUN-2000; 2000US-0215435.
07-JUL-2000; 2000US-0216447.
07-JUL-2000; 2000US-0216880.
11-JUL-2000; 2000US-0214887.
11-JUL-2000; 2000US-0214887.
11-JUL-2000; 2000US-0214887.
14-JUL-2000; 2000US-0212496.
14-JUL-2000; 2000US-0224518.
14-JUL-2000; 2000US-0225134.
15-SEP-2000; 2000US-0229134.
10-SEP-2000; 2000US-0229134.
10-SEP-2000; 2000US-0229134.
10-SEP-2000; 2000US-023124.
10-SEP-2000; 2000US-023124.
10-SEP-2000; 2000US-023124.
10-SEP-2000; 2000US-023134.
11-SEP-2000; 2000US-023134.
11-SEP-2000; 2000US-023134.
11-SEP-2000; 2000US-0231399.
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20000S-0231244
20000S-02314143
20000S-02314113
20000S-023141143
20000S-0231968
20000S-0231968
20000S-023239
20000S-023239
20000S-023239
20000S-023239
20000S-0233063
20000S-0233063
20000S-0233063
20000S-0233063
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2000US-0241221.
2000US-0241785.
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2000US-0236368.
2000US-0236369.
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2000US-0237037
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27-SEP-2000;
29-SEP-2000;
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02-OCT-2000;
02-OCT-2000;
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02-OCT-2000;
13-OCT-2000;
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4-SEP-2000;
1-SEP-2000;
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26-SEP-2000;
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29-SEP-2000;
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20-OCT-2000;
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200005-0249211. 200005-0249212. 200005-0249213. 200005-0249214. 200005-0249215. 20000S-024669 2000US-0246610 2000US-0246610 2000US-0246611 2000US-0246613 2000US-0249207 2000US-0249208 2000US-0249208 2000US-0249300. 2000US-0250160. 2000US-0250391. 2000US-0251030. 2000US-0251988. 2000US-0256719. 2000US-0246476. 2000US-0246477. 2000US-0246478. 2000US-0246523. 2000US-0246524. 2000US-0246525. 2000US-0246526. 2000US-0246527. 2000US-0246528. 2000US-0249245. 2000US-0249264. 2000US-0249265. 2000US-0249297 2000US-0249299 2000US-0246474 2000US-0246475 2000US-0249217 2000US-0249218 20 OCT - 2000; 20 OCT 11 - DEC - 2000; 01 - DEC - 2000; 05 - DEC - 2000; 05 - DEC - 2000; 06 - DEC - 2000; 08 - DEC - 2000; 08 - DEC - 2000; 17-NOV-2000; 17-NOV-2000; 05-JAN-2001; 

(HUMA-) HUMAN GENOME SCI INC

Ruben SM Rosen CA, Barash SC,

WPI; 2001-465570/50

plated nucleic acid molecule encoding a reproductive system antigen used in preventing, treating or ameliorating a medical condition Isolated 1.5

Disclosure; SEQ ID NO 9859; 1297pp + Sequence Listing; English.

The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention.

BP; 2518 A; 3387 C; 2921 G; 2002 T; 0 other; Sequence 10828 ö

Gaps

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0.93; ohes 71; Indels

Pred. No. 0.93 0; Mismatches

53.3%;

81; Conservative

Best Local Similarity Matches 81; Conserv

24

g ò

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Gaps

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Indels

Length 10828;

DB 22; 39;

1.8; Mismatches 84

gtgggaagggtctgggcctggcaggacctgggctggggtctccttggccctgctgtgtgc 143 

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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                           Sequence 357 BP; 56 A; 218 C; 22 G; 61 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences.
 Score 38.6;
Pred. No. 1.
 10.48;
61.48;
                                                                                                     AAI81967 standard; cDNA; 357
                                                                                                                                                                                                                                                                                      Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                       26-FEB-2001; 2001WO-US04927
                                                                                                                                                                                                                                                   28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
                                                                                                                                 (first entry)
              Conservative
                                                                                                                                                                                                                                                                                                   WPI; 2001-514838/56.
      Similarity
                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                          P-PSDB; AA002036
                                                                                                                                                                                                            WO200164835-A2.
                                                                                                                                                                                               Homo sapiens.
                                                                                                                                06-NOV-2001
             62;
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Query Match
                                                                                                                  AAI81967;
                                                                                                                                                                                                                                                                                                                                       disorders
       Local
      Best Loca
Matches
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AAI81967/CID AAI8:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 2027; 1399pp + Sequence Listing; English.
                                                                               10317 GGGGGGGGGGGGGGGGGGGGGGGGCACCGGCCTGG 10277
    64 ggcgggagggggggctgtgggaagggtctgggcctgg 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human polynucleotide SEQ ID NO 2027
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10.4%; Score 38.4; DB 22; Length 357;

**Ouery Match** 

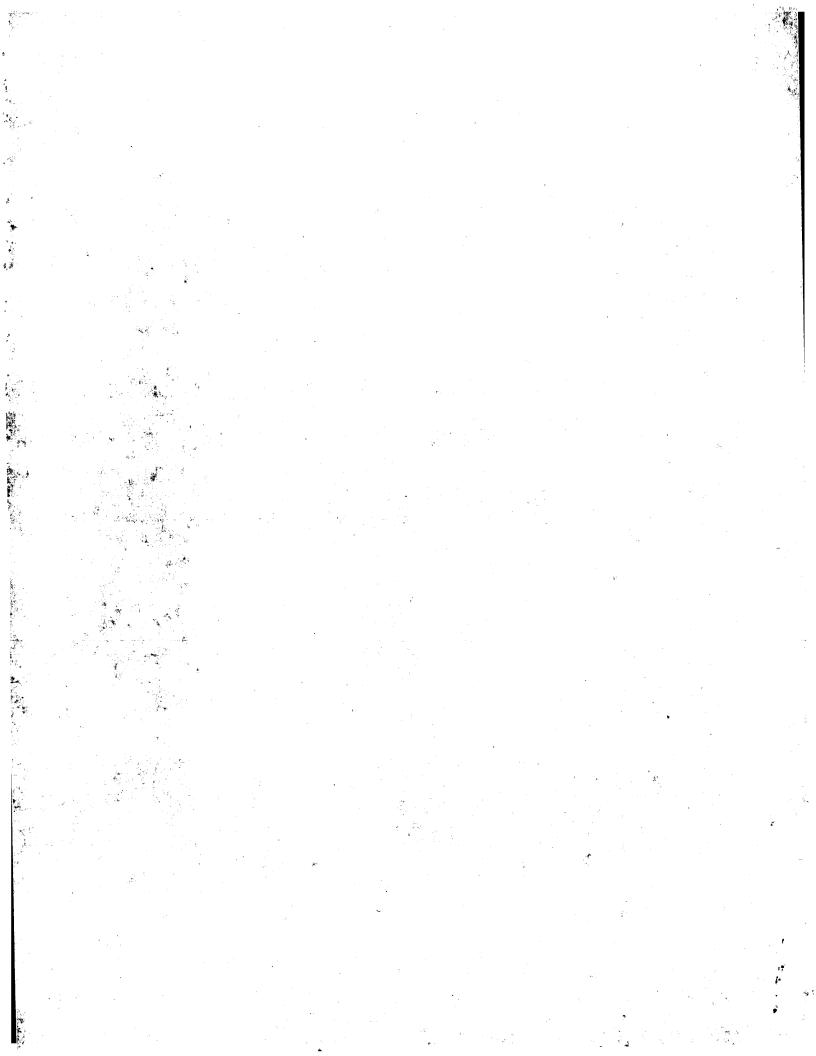
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AAA00010 to AAA02716 represent polynucleotides isolated from cDNA libraries constructed from human colon cancer cell lines. The present livention also describes a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived. The polynucleotides sequences can be used in a method for detecting differentially expressed genes correlated with a cancerous state of a mammalian cell. The polynucleotides can also be used as probes for detecting and mapping related genes. They can be used in diagnosis and prognosis of diseases and disorders (e.g. identification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polynucleotide library used to determine cancerous states of mammalian
                                                                                                                                                                                                                   Human colon cancer cell line polynucleotide sequence SEQ ID NO:2475.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sudduth-Klinger J;
                                                                                                                                                                                                                                                   Human; colon cancer; tumour; diagnosis; gene expression product;
probe; detection; cancerous state; metastasis; identification;
breast cancer; oestrogen receptor-positive breast cancer; therapy;
oestrogen receptor-negative breast cancer; lung cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escobedo J, Innis MA, García PD, Sudduth-Klinger
Jiese K, Randazzo F, Kennedy GC, Pot D, Kassam A;
nanac R, Crkvenjakov R, Dickson M, Drmanac S, Lab
Kita D, García V, Jones LW, Stache-Crain B;
144 tttgcggcaatgctgggtgctgtgactctcgg 175
                          148 TTGGGGAGAGTGGGGGGGGCAGTGGTTGTGGG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 994; 1097pp; English.
                                                                                                                AAA02484 standard; cDNA; 1000 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0085696.
98US-0105234.
98US-0105877.
                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US10602,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0085426
                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , Glese K,
Drmanac R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leshkowitz D, Kita D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-126369/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Williams LT, Reinhard C, G
                                                                                                                                                                                   19-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                        WO9958675-A2
                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                          18-NOV-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                          13-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-0CT-1998
27-0CT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-MAY-1998
                                                                                                                                                  AAA02484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-MAY-
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the bovine viral diarrhea virus (BVDV) genome. The primer is used to
illustrate the nucleic acid analysis methods of the invention. The
methods are used for sequencing a nucleic acid in a mixture comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid analysis methods for simultaneously analysing multiple nucleic acid regions for diagnosis and differentiation of pathological organisms comprises sequencing the nucleic acids in the reaction mixture -
pre-metastatic or metastatic cancerous states, stages of cancer, or responsiveness of cancer to therapy). This is particularly for breast cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-negative breast cancer, lung cancer, and colon cancer.
                                                                                                                                                                                                                                                                                                                           009
                                                                                                                                                                         gtgggaagggtctgggcctggcaggacctgggctggggtctccttggccctgctgtgtgc 143
                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnosis; pathological organism; detect; ss.
                                                                                                                                                                                                                                                                                                                           421 ggggggngcnnggnggggggggggggggnngggnggaggcgngggggggngn
                                                                                                                                                                                                                                                   144 tttgcggcaatgctgggtgctgtgactctcggataacctggagatccctgcttttgggcg
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0
                                                                                                   Length 1000;
                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Primer used in the analysis of a BVDV genome fragment.
                                                               Sequence 1000 BP; 21 A; 53 C; 574 G; 22 T; 330 other;
                                                                                                  Score 38.2; DB 21;
Pred. No. 1.3;
0; Mismatches 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; Page 23; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                           BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BIOI-) BIO-ID DIAGNOSTIC INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0165264.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bovine viral diarrhea virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-CA00915
                                                                                                      10.3%;
36.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA38184 standard; DNA; 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                               91; Conservative
                                                                                                                                                                                                                                                                                                                                                       gaagectgetg 274
                                                                                                                                                                                                                                                                                                                                                                              gangggnggng 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-303800/26
                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vinayagamoorthy T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200020628-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA38184;
                                                                                                       Query Match
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                                                                                                                   Best Loca
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two nucleic acid target sequences. The methods are used for simultaneously analysing multiple nucleic acid regions in a single reaction. This can allow the reliable diagnosis and differentiation of pathological organisms. The methods can be adapted to use a series of pathological organisms. The methods can be adapted to use a series of primers with additional sequences which allows the size of the amplified region to be increased. The technique is especially useful when the usual sequence of the region to be detected is known and the assay is being service out to confirm its presence e.g. to rule out a falsely positive amplification reaction or to distinguish subsets of an organism of interest or allelic forms of a gene associated with a disease or predisposition to a disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a primer used in the analysis of a fragment of the bovine viral diarrhea virus (BVDV) genome. The primer is used to illustrate the nucleic acid analysis methods of the invention. The methods are used for sequencing a nucleic acid in a mixture comprising two nucleic acid target sequences. The methods are used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid analysis methods for simultaneously analysing multiple nucleic acid regions for diagnosis and differentiation of pathological organisms comprises sequencing the nucleic acids in the reaction mixture -
                                                                                                                                                                                                                                                                                                                                        ggcctgtgggaagggtctgggcctggcaggacctgggctggggtctccttggccctgctg 138
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Primer; bovine viral diarrhea virus; BVDV; nucleic acid analysis; diagnosis; pathological organism; detect; ss.
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                                                                                                                                                                                                                                               Length 318;
                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in the analysis of a BVDV genome fragment.
                                                                                                                                                                                                                                              Score 37.6; DB 21;
Pred. No. 1.5;
0; Mismatches 54;
                                                                                                                                                                                                 Sequence 318 BP; 3 A; 3 C; 306 G; 6 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP
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                                                                                                                                                                                                                                                    10.2%;
56.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovine viral diarrhea virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA38185 standard; DNA; 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                  Local Similarity 56.5
nes 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-303800/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vinayagamoorthy T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200020628-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                             139 tgtg 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           307 tgtg 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA38185;
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Matches
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simultaneously analysing multiple nucleic acid regions in a single reaction. This can allow the reliable diagnosis and differentiation of pathological organisms. The methods can be adapted to use a series of primers with additional sequences which allows the size of the amplified region to be increased. The technique is especially useful when the usual carried out to confirm its presence e.g. to rule out a falsely positive amplification reaction or to distinguish subsets of an organism of interest or allelic forms of a gene associated with a disease or predisposition to a disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or
                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                   21; Length 320;
                                                                                                                                                                                                                                                                                                                                                     79 ggcctgtgggaagggtctgggcctggcaggacctggggctggggtctcc 126
                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding novel human diagnostic protein #3242.
                                                                                                                                                                                                                                                                44;
                                                                                                                                                                              Sequence 320 BP; 4 A; 6 C; 308 G; 2 T; 0 other;
                                                                                                                                                                                                                                   DB
                                                                                                                                                                                                                              10.2%; Score 37.6; D
59.3%; Pred. No. 1.5;
iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAS67438 standard; cDNA; 921
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAR-2001; 2001WO-US08631.
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23-AUG-2000; 2000US-0649167
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                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                         64;
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                                                                                                                                                                                                                           Query Match
Best Local Si
Matches 64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
AAS67438/C
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    quantitating a polypeptide in tissue, as molecular weight markers and as food supplement. (IT) and its blunding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polyuculeotide sequences have applications in responsible for genetic disorders or other traits to assess blodiversity and to produce other types of data and products dependent on DNA and diagnostic coding sequences ASS6197-AAS94564 represent novel human Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from Wipo at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    694 GCTGGGAGGCGGGGGCCGCGGGGCCCGGGGGCGCCCCGCGAGGCCGAGGC 635
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                  Score 37.4; DB 23; Length 921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92 ggtctgggcctggcaggacctgggctggggtctccttggccctgctgtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       634 GGGGGGGTCGGCGCAGGGAGGCTGCCTTCCCCTGCGCAGTGCTGC 584
                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                             Sequence 921 BP; 147 A; 345 C; 318 G; 111 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                             46;
                                                                                                                                                                                                                                                                                                                                                     10.1%; Score J., 58 6%; Pred. No. 2.1; 58 6%; O: Mismatches
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Job time: 9132 sec
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Best Local Similarity
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8.56666666666666888
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AC074220 Mus muscu AC102804 Homo sapi AC105291 Rattus no 166494 Sequence 14 U05240 Aryctologus AC023197 Mus muscu AC095701 Rattus no AC095701 Rattus no AC10581 Mus muscu AC10581 Mus muscu AC10589 Mus muscu AC106660 Mus muscu AC10569 Mus muscu AC10569 Homo sapi AC10154 Mus muscu AC10569 Homo sapi AC10154 Mus muscu AC022598 Homo sapi AC052595 Homo sapi AC095301 Rattus no AC027682 Homo sapi AC095301 Rattus no AC027682 Homo sapi AC095301 Rattus no AC07682 Homo sapi AC10595 Rattus no AC07682 Rattus no AC0669 Rattus no AC07682 Rattus no AC0669 Rattus no AC0669 Rattus no AC0669 Rattus no AC06693377 Homo sapi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus chromosome 17 clone RP23-76116 strain C57BL6/J, WORKING DRAFT SEQUENCE, 38 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 89855)
Han, J., Montgomery, K. T., Grills, G., Lee, E., Long, J., Pomerantz, R., Ioshikhes, I. P., Shim, C., Decker, J., Thomas, E., Perera, A., High Throughput Mouse Sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2. (bases 1 to 89855)
Han,J., Montgomery,K.T., Grills,G., Lee,E., Long,J., Pomerantz,R.,
Thonshikhes,I.P., Shim,C., Decker,J., Thomas,E., Perera,A.,
Gordon,M., Goltz,J.S. and Kucherlapati,R.
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AC026508 H
AC022783 AC079640 M
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AC105985
AC021584
AC074204
AC07610
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   AC074220
AC102804
AC102804
CC005204
AC0052137
AC02137
AC024865
AC02525
AC100281
AC095175
AC09757
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AC095300
AC027682
AC087563
CNS06EET
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AC107595
AC107595
AC087337
AC01222
AC018939
AC026508
AC026508
AC079640
AC107946
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HTG: HTGS_PHASE1; HTGS_DRAFT
                                               7218
1396
141892
236301
163525
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81767
144979
51119
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192182
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83296
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   999.6
113.7.7.6
113.6
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All repeats were identified using Repeatwasker.
                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 53178)
Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo. sapiens chromosome 18; clone RP11-605C5
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* sequencing reads that have not been assembled into
contigs. Runs of N are used to separate the reads
and the order in which they appear is completely
arbitrary. Low-pass sequence asmpling is useful for
identifying clones that may be gene-rich and allows
overlap relationships among clones to be deduced.
However, it should not be assumed that this clone
will be sequenced to completion. In the event that
the record is updated, the accession number will
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Center code: WIBR
Web Site: http://www.seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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18725: contig of 719 bp in length
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11359: contig of 722 bp in length
11459: gap of 100 bp
12174: contig of 715 bp in length
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13.7%; Score 50.8; DB 2; Length 5
Best Local Similarity 49.0%; Pred. No. 0.082;
Matches 97; Conservative 0; Mismatches 101; Indels
                                                                                                                                                                                                               3777 37816: gap of 100 bp 37817 38525: contig of 709 bp in length 38525 app of 100 bp 38626 app of 100 bp 38626 app of 100 bp 39410 40133: contig of 724 bp in length 40134 40233: gap of 100 bp 40234 40950: contig of 617 bp in length 40851 40950: contig of 617 bp in length 40851 40950: contig of 733 bp in length 40951 41683: contig of 733 bp in length
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/clone="RP11-605C5"
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                                                                                                                                                                                                                                                             39811 bp DNA linear HTG 12-JAN-2002 Rattus norvegicus clone CH230-212K18, *** SEQUENCING IN PROGRESS AC105591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (12-0AN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                      Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ಧ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc.help@bcm.tmc.edu
Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center clone name: CH230-212K18
                                                                                                                AC106591.1 GI:18139115
HTG; HTGS_PHASE1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
2 (bases 1 to 39811)
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                                                                                                                                                                                Rattus norvegicus
                                                                                                                                                             Norway rat.
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                   LOCUS
AC106591/c
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                                                                                      ACCESSION
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 25 contigs. The true order of the places is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as This record will be updated with the finished sequence as soon as it is available and the accession number will
Consensus quality: 46037 bases at least Q20
Estimated insert size: 24639; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 0.3x in Q20 bases; sum-of-contigs estimation
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/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone="CH230-212x18"
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gap of unknown l
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contig of 1831 b
gap of unknown l
contig of 2193 b
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Location/Qualifiers
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       rabbit.
Oryctolagus cuniculus
                                                                                                                                                                                                                        /sex="male"
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Best Local Similarity 48.09
Matches 141; Conservative
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Oryctolagus cuniculus preproacrosin MRNA, complete cds.
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                                                                             79 ggcctgtgggaagggtctgggcctggcaggacctgggctgggtctccttggccctgctg 138
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                                      126 cttggccctgctgtgtgtttgcggcaatgctgggtgctgtgactctcggataacctgga
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                     0;
   Length 39811;
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Best Local Similarity 0.9%; Pred. No. 0.13;
Matches 3; Conservative 214; Mismatches 135; Indels
                                                                                                                                                                                          linear
                      Indels
                                                                                                                                                                                                                                                                        1 (bases 1 to 7218)
Dorner,F., Scheiflinger,F. and Falkner,F.Gunter. Recombinant fowlpox virus
Patent: US 5570367-A 14 23-SEP-1997;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                         368
                      64;
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   Score 50.6; DB 2
Pred. No. 0.094;
0; Mismatches 6
                                                                                                                                   Db 36003 GGTGGTCGGCGCGCGCGCGGTCGGGCTC 35971
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/ vcusure_ropest interliated
/product="preproactosin"
/protein_id="AAA61630.1"
/db_xref="Gi1451842"
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/db_xref="Gi14518
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Submitted (15-JAM-1994) Richard T. Richardson, Cell Biology and
Anatomy, University of North Carolina, Room 210 Taylor Hall, Chapel
Hill, NC 27599, USA
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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                                                                                                Manufactury 10 (1986)

Richardson, R.T. and O'Rand, M.G. (1981)

Cloning and sequencing of cDNAs for rabbit preproacrosin and social related CDNA for rabbit preproacrosin-related CDNA for contin. Biophys. Acta 1219 (1), 215-218 (1994) 9436861

2. (bases 1 to 1396)

Richardson, R.T.
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/clone_lib="cDNA custom prepared by Clontech"
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/codon_start=1
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/strain="New Zealand White"
/Ab_xref="taxon:9986"
/clone="1033,412,1021,a51"
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Pred. No. 0.28;
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/EC_number="3.4.21.10"
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/EC_number="3.4.21.10"
/evidence=experimental
/product="proacrosin"
1315. .1396
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5787: crr
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8376: con
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9227: cor
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31482: con
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Direct Submission

All repeats were identified using Repeathasker:

Submitted (09-FEB-2000) Whitehead Institute/MIT Center for Genome On Mar 16, 2000 this sequence version replaced gi:6957784.

Smit, A.F. A. & Green, P. (1996-1997)

http://ftp:genome.washington.edu/RM/Repeathasker.html

Center: Whitehead Institute/ MIT Center for Genome Center code: WIRE code: 
                                                                                                                                                                                                                                                                                                        HTG 16-MAR-2000
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 141892)
AC023197
Mus musculus clone RP22-239F2, LOW-PASS SEQUENCE SAMPLING
                                                                                 259 tacaggaagcctgctgcgaaatgaagagttggccagggaaagcatggcgtgcag 312
                                                                                                                     * NOTE: This record contains 155 individual
    * sequencing reads that have not been assembled into
    * contigor. Runs of N are used to separate the reads
    * and the order in which they appear is completely
    * arbitrary. Low-pass sequence sampling is useful for
    * identifying clones that may be gene-rich and allows
    * overlap relationships among clones to be deduced.
    * However, it should not be assumed that this clone
    * will be sequenced to completion. In the event that
    * the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 756: gap of 100 bp
1510: contig of 754 bp in length
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Unpublished
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HTG; HTGS_PHASE0.
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AUTHORS
TITLE
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TITLE JOURNAL COMMENT

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38 53907: gap of 100 bp 100 bp
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34071: contig of 769 bp in length

72 34171: gap of 100 bp

72 34931: contig of 760 bp in length

32 35031: gap of 100 bp

35795: contig of 764 bp in length

3640: contig of 745 bp in length
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59965: gap of 100 bp
60707: contig of 742 bp in length
60807: gap of 100 bp
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45252: contig of 773 bp in length
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46095: contig of 743 bp in length
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46960: contig of 765 bp in length
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47912: contig of 752 bp in length
47912: gap of 100 bp
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JOURNAL REFERENCE

1 (bases 1 to 225301)

Standary C. Addo-Oduola, B., Ali-Osman, F. R., Allen, C., Alabrooks, S. L., Amaratunge, H.C., Are, J. R., Banks, T., Barbaria, J., Balager, K., Blankenburg, K., Bonnin, D., Bouck, J., Banger, K., Blankenburg, K., Bonnin, D., Bouck, J., Banger, K., Blankenburg, K., Bonnin, D., Bouck, J., Blanger, K., Blankenburg, K., Bonnin, D., Bouck, S. R., Chacko, J., Chavez, D., Carron, T.F., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Burch, P., Burkett, C., Burchil, K.L., Byrd, N.C., Carron, T.F., Crater, M., Cavazos, S.R., Chacko, J., Chavez, D., Chard, C., Chon, G., Chan, C., Chor, L., Chon, C., Chon, C., Chan, C., Chon, C., 236301 bp DNA linear HTG 12-JAN-2002 Eattus norvegicus clone CH230-6H1, \*\*\* SEQUENCING IN PROGRESS \*\*\*, S7 unordered pieces. Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 139 tgtgctttgcggcaatgctgggtgctgtgactctcggataacctggagatccctgcttt 198 ggcctgtgggaagggtctgggcctggcaggacctgggctggggtctccttggccctgctg 138 94539 NNGAGGGGGNNGGGAACGGAATCAGCNTTTAACAGNTGAATCAT 94495 259 tacaggaagcctgctgcgaaatgaagagttggccagggaaagcat 303 AC094865.4 GI:17941649 HTG; HTGS\_PHASE1. Norway rat DEFINITION ORGANISM 199 VERSION KEYWORDS SOURCE REFERENCE AUTHORS 4 ACCESSION RESULT - AC094865 qq οp δ

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Worley, K.C.

Direct Submission
Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Dec 20, 2001 this sequence version replaced gi:17062165.

Center: Baylor_College of Medicine
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NOTE: This is a 'working draft' sequence. It currently consists of 57 contigs. The true order of the pieces is an other order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                         Consensus quality: 201553 bases at least 040 Consensus quality: 208709 bases at least 030 Consensus quality: 214444 bases at least 030 Estimated Ansert size: 213429; sum-of-contigs estimation Quality coverage: 0x in 020 bases; agarose-fp estimation Quality coverage: 2.9x in 020 bases; sum-of-contigs estimation
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Registry, D. M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Adio-Oduola, B., Banks, T., Barbaria, J., Banton, S. L., Adams, C., Adio-Oduola, B., Bandin, D., Bouck, J., Bunkaratuge, M., Blown, M., Brown, M., Brown, M., Brown, M., Brown, E., Bornin, D., Bouck, J., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Burter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Carroll, J., Dathone, S.R., David, R., David, R., David, C.D., Cox, C., Coyle, M.D., Dathone, S.R., David, R., David, R., David, C.D., Cox, C., Davy, Carroll, L., Dind, H.H., Douthwaite, K.J., Draper, H., David, R., Delgado, O., Dann, A.L., Ding, T., Dinh, H.H., Douthwaite, K.J., Draper, H., Escotto, M., Falls, T., Earnhart, C., Edgar, D., Edwards, C. C., Elhaj, C., Escotto, M., Falls, T., Rerraguto, D., Flagg, N., Ford, J., Escatz, N., Gill, R., Gorrell, J.H., Gorrell, J.H., Guevara, W., Gunarathe, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Houlloway, C., Hannitton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Jackson, L.E., Jacobson, E., Rell, S., Huber, J., Hulber, S., Honson, E., Vall, R., Loliver, S., Hulber, S., Jackson, L.E., Jacobson, E., Edl, S., Lichtarge, O., Lieu, C., Liu, J., Liu, M., Lade, H., Lozado, R.J., Li, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martinez, E., Massey, E., Mawhiney, E., Martinez, E., Massey, E., Manker, C., Miner, C., Miner, C., Miner, C., Mordon, M., Nguyen, N., Ngu
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163525 bp DNA linear HTG 20-DEC-2001

Rattus norvegicus clone CH230-9B18, *** SEQUENCING IN PROGRESS ***, 62 unordered pieces.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Length 236301;
   Score 48.8; DB 2; Length 2
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0; Mismatches 117; Indels
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KEYWORDS
SOURCE
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 62 contigs. The true order of the pleces consists of 62 contigs. The true order of the pleces arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                    Consensus quality: 135093 bases at least 040 Consensus quality: 143387 bases at least 030 Consensus quality: 149395 bases at least 020 Estimated insert size: 131571; sum-of-contigs estimation Quality coverage: 0x in 020 bases; agarose-fp estimation Quality coverage: 2.3x in 020 bases; sum-of-contigs estimation
                                                                                                            Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Dec 20, 2001 this Sequence version replaced gi:15627321.

Center: Baylor College of Medicine Center code: BCM
Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstock,G. and Gibbs,R.
Direct Submission
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                                                                                                                                                                                                                                                                           Center clone name: CH230-9B18
----- Summary Statistics
Assembly program: Phrap; version 0.990329First call
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6386: gap of unknown length
11837: contig of 5451 bp in length
11937: gap of unknown length
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Contact: hgsc-help@bcm.tmc.edu
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Pred. No. 0.28;
0; Mismatches 63; Indels 0;
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NOTE: This is a 'working draft' sequence. It currently consists of 87 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                             Updates 1 to 148921)

Worley, K.C.
Worley, K.C.

Worley, K.C.

Worley and Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Dec 20, 2001 this sequence version replaced 9::15625779.

Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                          Consensus quality: 117844 bases at least 040 consensus quality: 130606 bases at least 030 consensus quality: 138533 bases at least 020 Estimated insert size: 78668; sum-of-contigs estimation Quality coverage: 0.x in 020 bases; agarose-fp estimation quality coverage: 0.9x in 020 bases; sum-of-contigs estimation
Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstock,G. and Gibbs,R.
Direct Submission
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Contact: hgsc-help@bcm.tmc.edu
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Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                      * NOTE: This record contains 45 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
the record is updated, the accession number will
               p of 100 bp in length in contig of 946 bp in length in p of 100 bp in length p of 100 bp in length in contig of 941 bp in length in contig of 941 bp in length
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Pred. No. 0.44;
0; Mismatches 211; Indels 0;
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8700 c 8777 g 12424 t 5348 others
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43642: contig of 994 bp in length
42: gap of 100 bp
44701: contig of 959 bp in length
301: gap of 100 bp
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35205: contig of 884 bp in length
365: gap of 100 bp
36272: contig of 967 bp in length
373: gap of 100 bp
373: contig of 988 bp in length
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38362: contig of 902 bp in length

38462: gap of 100 bp

39425: contig of 963 bp in length

39525: gap of 100 bp
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41461: contig of 970 bp in length
561: gap of 100 bp
42548: contig of 987 bp in length
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/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP23-94114"
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NCE I (bases I to 199336)

NURLAIN, Adamas, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C.,

Alsbrooks, S.L., Amaratuge, H.C., Are, J.R., Banks, T., Barbaria, J.,

Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bouck, J.,

Bowie, S., Brikett, C., Burrell, K.L., Brydn, N.P., Buyah, C.,

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Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F.,

Burch, D., Dathorne, S.R., Checko, J., Cleveland, C.D., Cox, C.,

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Coyle, M.D., Dathorne, S.R., Checko, J., Chevez, D., Chen, S.,

Denn, A.L., Ding, Y., Dinh, H. H., Douthwaite, K. J., Dragado, O.,

Blad, C., Escotto, M., Farls, T., Perraguto, D., Flaga, N., Ford, J.,

Elhaj, C., Escotto, M., Earls, T., Ferraguto, D., Flaga, N., Ford, J.,

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Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A.,

Hernandez, J., Harrishor, E., Bodoson, J., Garcia, M., Holloway, C.,

Joudah, S., Karlsson, E., Howard, S., Hane, J., Hane, J.,

Joudah, S., Karlsson, E., Lichtarge, O., Lied, C., Liu, J., Liu, M.,

Louiseged, H., Lozado, R.J., Lu, X., Lucier, M., Lotle, E., Luna, R.,

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Martinez, E., Massey, E., Mawhiney, E., McLeol, M. P., Meador, M.,

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Martinez, E., Massey, E., Mawhiney, E., McKerson, E., Noguen, A., Nguyen, M., Moser, M., Moser, M., Moser, M., Moser, M., Woll, D., Vallalon, D., Vinson, R.,

Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Sutcon, A., Stone, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N.,

Ruis, S., Wallson, S., Walliams, G., Walliamson, A., Wallerson, D., Vallalon, D., Vallalon, D., Vallalon, D., Vallalon, S., Welley, M., Tang, W., Taylor, T., Telfrod, B., Thomas, N.,

Ruis, S., Savery, G., Scherer, S., Scott, G., Shen, H., Tansey, J., Tang, W., Tang, W., Tang, W., Wall, M., Wall, M.
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           DNA linear HTG 20-DEC-2001
                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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On Dec 20, 2001 this sequence version replaced gi:17062167.
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Rattus norvegicus clone CH230-6J18,
57 unordered pieces.
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2 (bases 1 to 199536)
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Direct Submission
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NOTE: This is a 'working draft' sequence. It currently consists of 57 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                    Consensus quality: 175647 bases at least 040 Consensus quality: 183106 bases at least 030 Consensus quality: 188319 bases at least 030 Estimated insert size: 181273; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agazose-fp estimation Quality coverage: 2.9x in 020 bases; sum-of-contigs estimation
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Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Binger, K., Blankenburg, K., Bonnin, D., Bouck, J., Busch, M., Brown, E., Brown, M., Bryant, N.P., Burks, T., Barbaria, J., Bowie, S., Britera, M., Brown, E., Brown, M., Bryant, N.P., Bunck, J.C., Carron, T.F., Burch, P., Burkett, C., Burrell, K.L., Burd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, G., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy, Carroll, L., Dederich, D.A., Delaney, K.R., Delaney, K.R., Dagado, O., Davy, Carroll, L., Dederich, D.A., Delaney, K.R., Dagado, O., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flags, M., Ford, J., Forster, P., Frantz, P., Gabisl, A., Gao, J., Garcia, M., Ford, J., Forster, P., Frantz, P., Gabisl, A., Gao, J., Garcia, M., Ford, J., Jackson, L.E., Jackson, E., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howaris, C., Hartis, K., Hart, M., Havlak, P., Lueier, M., Liu, W., Liu, W., Liu, J., Liu, J
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Submitted (16-SEP-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Dec 20, 2001 this sequence version replaced gi:15625729.
                                                                                                                                                                                                                                                                                                                                    ACU95175 107781 bp DNA linear HTG 20-DEC-2001 Rattus norvegicus clone CH230-8J16, *** SEQUENCING IN PROGRESS ***, 60 unordered pieces.
                                    DD 197572 TCACGCGCGCTGGGGCGAACCCGGTGCCATCACCGCGGGAAGGCTTGGTGCCCCCC 197513
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
185 agatccctgcttttgggcgaatccgggggtagttgctcatcaagactagaggtgggggtg 244
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* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft' sequence. It currently

* consists of 60 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N. but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                               Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 0.8x in Q20 bases; sum-of-contigs estimation
                                                                                                                   Consensus quality: 73837 bases at least Q40
Consensus quality: 87577 bases at least Q30
Consensus quality: 95671 bases at least Q20
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AC079431 300695 bp DNA 11near HTG 01-SEP-2000 Mus musculus chromosome 16 clone RP23-1J12, WORKING DRAFT SEQUENCE, AC079431
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Consensus quality: 164936 bases at least 030
Consensus quality: 214345 bases at least 030
Consensus quality: 214345 bases at least 030
Consensus quality: 214345 bases at least 030
Estimated insert size: 293095; sum-of-contigs estimation
Quality coverage: 3.01 in 020 bases; agarose-fp estimation
* NOTE: This is a working draft' sequence. It currently
* consists of 77 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (01-SEP-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 300695)
DOE Joint Genome Institute.
Sequencing of Mouse
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Center clone name: RPCI-23_1J12
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HTG: HTGS_PHASE1; HTGS_DRAFT.
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Mus musculus clone RP23-16704, LOW-PASS SEQUENCE SAMPLING.
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gap of

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arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will 95.6 9555; ago for 100 bp 100 100 bp of 690 bp in length 100 bp f 694 bp in length 100 bp f 686 bp in length 100 bp f 717 bp in length 717: contig of 717 bp in length 100 bp f 700 bp in length 100 bp f 682 bp in length 100 bp f 679 bp in length in length 0 bp 695 bp in length 10 bp 693 bp in length 00 bp 687 bp 1 100 bp of 715 bp 100 00. 001 1 7180: gap of 100 1 7867: contig of 60 8 7967: gap of 100 8 8662: contig of 60 3 8762: gap of 100 3 8762: gap of 100 3 8762: gap of 100 817: gap of 100 1507: contig of contig of contig of contig of contig of ō contig of contig of contig 7: gap of 4704: con 9: gap of 6298: con 4804: gap of 5519: con 5619: gap of 6398: gap of 7080: cor 1607: gap of 2301: co 2401: gap of 3087: co 3187; gap of 3887; cor 3987: be preserved.

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41 45340: gap of 100 bp

41 46027: contig of 687 bp in length

428 46127: gap of 100 bp

84 46799: contig of 672 bp in length

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85 4764: contig of 685 bp in length

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I (bases 1 to 192182)

Ribbooks, S. L., Amaratunge, H.C., Aer, J.R., Banks, T., Barbaria, J., Barbario, J., Barbaria, J., Barbario, B., Bankenburg, K., Bonnin, D., Bouck, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Burett, C., Burrell, K. L., Byrd, N.C., Carron, T.F., Byrdert, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S. R., Chacko, J., Chavez, D., Chen, G., Chen, Z., Chendry, J., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S. R., David, R., Davila, M.L., Durger, Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flaggi, N., Ford, J., Ellaj, C., Escotto, M., Falls, T., Ferraguto, D., Flaggi, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Garria, A., Garner, T., Foster, P., Frantz, P., Gabisi, A., Garcia, A., Garner, T., Foster, P., Harnandez, J., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Jackson, B., Jak, Y., Johnson, R., Johnson, R., Johnson, R., Joudh, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Ju, J., Li, J., Li, J., Li, J., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, M., Lozado, R.J., Lu, X., Lucier, R., Marlinez, E., Massey, E., Mawhiney, E., Micheod, M. P., Meador, M., Monten, M., Monten, M., Neule, N., Neules, D., Neutson, J., Neutson, N., Neuven, N., Neuver, N., Neuver,
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Rattus norvegicus clone CH230-4A13, *** SEQUENCING IN PROGRESS ***,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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40.1%;
                  Query Match 12.79
Best Local Similarity 40.13
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Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Walliams,G., Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley, K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Direct Submission

1. Unpublished
2. Chases 1 to 192182)
3. Worley, K.C.

2. Chases 1 to 192182)
3. Worley, K.C.

3. Unpublished
4. Chases 2 to 192182)
4. Chases 2 to 192182)
4. Chases 3 to 192182
4. Chases 3 to 192182
5. Samission
5. Chases 1 to 192182
6. Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
6. On Dec 20, 2001 this sequence version replaced gi:15624432.
6. Center code: Raching Center Conter Conter code: Redictine
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NOTE: This is a 'working draft' sequence. It currently consists of 94 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Consensus quality: 135751 bases at least 040
Consensus quality: 146003 bases at least 030
Consensus quality: 153797 bases at least 020
Estimated insert size: 123383; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agazose-fp estimation
Quality coverage: 2.1x in Q20 bases; sum-of-contigs estimation
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 1882)
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Strausberg, R.
Direct Submission
Submitted (04-SEP-2001) National Institutes of Health, Mammallan
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Contact: MGC help desk
Emall: cgapbs-rémail.nih.gov
Tissue Produrement: Jaffrey E. Green, M.D.
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       GenCore version 4.5
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cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
http://www.shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="mesmselaprcllfpllllbpllllpapkigpspagaeetDWVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LPSKCEVCKYVAVELKSAFEETGKTKEVIDTGYGILGGKGSGYKYTKSDIRLIEYTET
ICKRLLDYSLHKERTGSBRFARGMSETFETLHNLVHKGVKVVMDIPYELMNETSAEVA
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ASLGGKKSKKKRSGVKGSSSGSSKQRKELGGLGEDANAEEEEGVQKASPLPHSPPDEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF361644 11009 bp mRNA linear ROD 12-MAY-2001
Mus musculus putative retinoic acid-regulated protein mRNA,
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Glozak,M.A., Li.Y., Reuille,R. and Rogers,M.B.
                                                                                                                                                                             Clone distribution: MGC clone distribution information can be for
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 25 Row: j Column: 9.
Location/Qualifiers
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/db_xref="taxon:10090"
/cell_line="P19; derived from matings between C3H/He
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Glozak,M.A., Li,Y., Reuille,R. and Rogers,M.B.
Direct Submission
Submitted (15-MAR-2001) Biology, University of
E. Fowler Avenue, Tampa, FL 33620, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="RIKEN cDNA 1600025D17 gene"
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/db_xref="GI:15488836"
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SOURCE
ORGANISM
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AUTHORS
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ORIGIN
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TITLE
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AC074220 Hus musculus chromosome 17 clone RP23-76116 strain C57BL6/J, WORKING DRAFT SEQUENCE, 38 unordered pieces.
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et al., Dev. Biol., 170, 420)"
89. .919
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High Throughput Mouse Sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (20-JUL-2000) Department of Molecular Genetics, Albert Einstein College of Medicine Genome Center, 1300 Morris Park Ave., Bronx, NY 10461, USA On Apr 28, 2001 this sequence version replaced gi:11276104.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Han, J., Montgomery, K.T., Grills, G., Lee, E., Long, J., Pomerantz, R., Ioshikhes, I.P., Shim, C., Decker, J., Thomas, E., Perera, A., Gordon, M., Goltz, J.S. and Kucherlapati, R.
Direct Submission
females and male animals carrying an X chromosome derived
from a feral mouse (McBurney & Rogers, Dev. Biol., 89,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 89855)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                              /product="putative retinoic acid-regulated protein"
/protein_id="AAMK52494.1"
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*Consensus quality: 79355 at least Q20
*Consensus quality: 75365 at least Q30
*Consensus quality: 69022 at least Q40
Estimated insert size: agarose-FP - N/A
**Estimated insert size: 89115 - sum-of-contigs
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of unknown length
q of 907 bp in langth
of unknown length
g of 1633 bp in length
g of 1630 bp in length
g of 1001 bp in length
f unknown length
g of 1417 bp in length
f unknown length
g of 749 bp in length
                                                           contig of 907 bp in length is contig of 907 bp in length is gap of unknown length is gap of unknown length is gap of unknown length is contig of 1001 bp in length is contig of 1417 bp in length is gap of unknown length is contig of 749 bp in length is gap of unknown length is gap of unknown length is gap of unknown length is contig of 859 bp in length.
                          1817 bp in length
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70106. '38sembly_name:Contigl22"
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    89855 ...
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85769:
86770:
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88207:
88327:
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89855:
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                                                                                                                                                                                                                                                                                                                                        source
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agarose-FP - N/A 5.1\ x in Q20 bases; sum-of-contigs estimation
                                      NOTE: This is a 'working draft' sequence. It currently consists of 38 conties. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the conties are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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6: contig of 2720 bp in length
7: contig of 2720 bp in length
7: contig of 2014 bp in length
7: contig of 1981 bp in length
8: gap of unknown length
9: contig of 1981 bp in length
1: gap of unknown length
9: contig of 1752 bp in length
1: gap of unknown length
1: gap of unknown length
1: gap of unknown length
2: contig of 1614 bp in length
8: gap of unknown length
8: contig of 1614 bp in length
8: contig of 1614 bp in length
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contig of 2335 bp in length
gap of unknown length
contig of 2169 bp in length
gap of unknown length
contig of 1529 bp in length
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of 1665 bp in length
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of 1194 bp in length
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of 1922 bp in length
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gap of unknown 1
gap of unknown 1
contig of 5046 b
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contig of 3491 b
gap of unknown 1
gap of unknown 1
contig of 4598 b
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contig of 4588 b
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Oryza sativa
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S. Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Gupta, J., Haghighi, P., Hoó, J.E., Idol, J.R., Karlins, E., Larich, P., Lee-Lin, S.-O., Legaspi, R., Maduro, C.L., Maduro, V.B., Masiello, C., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Prasad, A., Shevchenko, Y.; Stantipop, S., Thomas, J.W., Thomas, P. J., Touchman, J. W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Zhang, L.—H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTG 19-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC097589 187142 bp DNA linear HTG 19-OCT-2C Sus scrofa clone RP44-78J22, WORKING DRAFT SEQUENCE, 4 unordered places. AC097589 AC097589 AC097589 HTG: HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (19-OCT-2001) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 consensus quality: 185160 bases at least Q40 Consensus quality: 185144 bases at least Q20 Insert size: 179000; agarose-fp Insert size: 179000; agarose-fp Insert size: 186842; sum-of-contigs Quality coverage: 10.12x in Q20 bases; agarose-fp Quality coverage: 9.70x in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                         100.0%; Score 25; DB 2; Length 89855; 100.0%; Pred. No. 0.16; 0; Mismatches 0; Indels 0
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      /note="assembly_name:Contigl19"
7470. .75963
7470. .75963
7470. .75964
7700e="assembly_name:Contigl18"
77926. .77936
77926. .79236
77927. .79236
7700e="assembly_name:Contigl16"
7927. .81332
7700e="assembly_name:Contigl15"
7700e="assembly_name:Contigl15"
7700e="assembly_name:Contigl16"
7700e="assembly_name:Contigl16"
81350. .81096
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Web site: http://www.nisc.nih.gov
Contact: nisc_mouse@nhgri.nih.gov
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Center clone name: 078J22
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Direct Submission
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AC107207 109963 bp DNA linear HTG 06-FEB-2002 Oryza sativa chromosome 3 clone OSJNBb0106M04, *** SEQUENCING IN PROGRESS ***, 7 unordered pieces.
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1 (bases 1 to 109963)

Buell,R., Hsiao,J., Zismann,V., Moffat,K.M., Hill,J., Brenner,M., Ciecko,A., Pai,G., Vanaken,S., Hansen,C., Utterbach,T., Feldblyum,T., Khalak,HG., Yuan,Q., Quackenbush,J., White,O., Salzberg,S. and Fraser,C.
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Submitted (16-JAN-2002) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
On Feb 6, 2002 this sequence version replaced gi:18158373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Pred. No. 19;
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40777 c 40348 g 51863
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/note="assembly_fragment"
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1. 15610
/note="assembly_fragment
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/note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone="RP44-78J22"
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AC107207.2 GI:18543002
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91.7%;
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Ouery Match 79.2
Best Local Similarity 91.3
Matches 21; Conservative
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Homo sapiens chromosome 5 clone CTB-35K5, WORKING DRAFT SEQUENCE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (06-OCT-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Feb 14, 2001 this sequence version replaced 91:9954634.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 184268)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 109963;
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                                                                                                                                            21690: contig of 21690 bp in length 21732: gap of unknown length 63992: contig of 42260 bp in length 64034: gap of unknown length 73846: contig of 9812 bp in length 73888: gap of unknown length 89053: contig of 15165 bp in length 89065: contig of 15165 bp in length 97762: contig of 8667 bp in length 97762: contig of 8667 bp in length 100079: gap of unknown length 100079: gap of unknown length 100079: gap of unknown length 100079: contig of 2235 bp in length 100079: gap of unknown length
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HTG: HTGS_PHASE2; HTGS_DRAFT; HTGS_ACTIVEFIN.
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Pred. No. 60;
0; Mismatches
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/organism="Oryza sativa"
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Center clone name: CIT978SKB_35K5
                                                                                                                                                                                                                                                                                                                                                                                                                   /cultivar="Nipponbare"
/sub_species="japonica"
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DOE Joint Genome Institute.
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Best Local Similarity 91.3
Matches 21; Conservative
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64035
73847
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AC011401
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ORGANISM
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ORIGIN
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JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT (AC011401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                  FEATURES
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Consensus quality: 173129 bases at least Q40
Consensus quality: 180377 bases at least Q30
Consensus quality: 180377 bases at least Q30
Consensus quality: 180377 bases at least Q30
Consensus quality: 180370 bases at least Q30
Estimated insert size: 200000; pulse field gel estimation
Coulity coverage: 6.62 in Q20 bases; pulse field gel estimation
Quality coverage: 7.22 in Q20 bases; pulse field gel estimation

* NOTE: This is a 'working draft' sequence. It currently
consists of 11 contigs. Gaps between the contigs
are represented as runs of N. The contigs estimation.

* NOTE: This is a 'working draft' sequence. It currently
consists of 11 contigs. Gaps between the sizes

* of the gaps between them are based on estimates that have
provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 121633 21732: gap of unknown length

* 23339 29438: gap of unknown length

* 23439 32379: contig of 15565 bp in length

* 47715 63279: contig of 15555 bp in length

* 47715 63279: contig of 15565 bp in length

* 63380 69838: contig of 15565 bp in length

* 63380 69838: contig of 15565 bp in length

* 63380 69838: contig of 15565 bp in length

* 69839 17417: contig of 1557 bp in length

* 63380 69838: contig of 1557 bp in length

* 63830 69838: contig of 1557 bp in length

* 63380 69838: contig of 1557 bp in length
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Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 186780)
Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M.,
Kadner,K., Miguel,T., Miller,C., Pitluck,S., Pollard,M.,
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Pred. No. 61;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gap of unknown length
contlg of 6459 bp in length
gap of unknown length
contlg of 1574 bp in length
gap of unknown length
contlg of 5907 bp in length
gap of unknown length
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40258 c 38925 g 51136 t 1001 others
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contig of 37532 bp in length
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/db_xref="taxon:9606"
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91.38;
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77519:
77619:
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Rojeski,H., TITLE Sequencing of JOURNAL Unpublished REFERENCE 2 (bases 1 AUTHORS Ricke,D.O. TITLE Large Scale	Rojeski,H., Subramanian,S. and Martin,C.H. Sequencing of human chromosome 5 Unpublished 2 (bases 1 to 186780) Ricke,D.O. Ricke,D.O. Large Scale Sequence Analysis and Annotation with the Sequence	repeat_region repeat_region repeat_region
Comparison I	Large State Sequence Analysis and Amnotation with the Cognition and Lysis (SCAN) System Unpublished	repeat_region
rly rly r, k	<pre>3 (Cases I to 100/80) Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M., Kadnerly,W., Miguel,T., Miller,C., Pitluck,S., Pollard,M., Rojeski,H., Subramanian,S. and Martin,C.H.</pre>	repeat_region repeat_region
tec	<pre>bmission (01-OCT-1998) Human Genome Center, DOE Joint Genome ( Lawrence Berkeley National Laboratory, MS 74-157,</pre>	reneat region
ce oin	Werkeley, CA 34/20, U.S.A. Sequence submitted by: DOE Joint Genome Institute.	repeat_region
	Location/Qualifiers 1186780	repeat_region
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		repeat_region
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repeat_region	complement(34863634) /rpt_family="L1"	repeat_region
repeat_region	3638 .3938 /rpt_family="Alu"	repeat_region
repeat_region	39213843 	repeat_region
reneat region	/ibt_cype=-dailuem //rpt_unit=-assassassassassassassassassassassassass	repeat_region
	Compression 1 = MIR2 =	repeat_region
	Comprement(77.5)	repeat_region
	Comptensity(vac)	repeat_region
repeat_region	Comprement(1999) //rpt_family="Alu"	misc_feature
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	/rpt_rype=randem /rpt_unit==	repeat_region
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	complement(78337932) /rpt_family="MSTC"	repeat_region
repeat_region	84928601 /rpt_family="Alu"	repeat_region
repeat_region	complement(94039676) /rpt_family="Alu"	repeat_region
repeat_region	complement(10100 .10257) /rpt_family="Alu" .	repeat_region
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repeat_region	1122411247 /note="(ATTC)6"	repeat_region
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		frame 2"	
.12811) .13169) .13889)	.16462) .16902) .18870) .18822)	u" 321577) u" .22011) u" excellent exon, u" u" excellent exon, u" u"	.29490)
/rpt_unit=A complement(12372. /rpt_family="L1" 12900. 13016 /rpt_family="Alu" complement(13084. /rpt_family="L1" /rpt_family="L1" /rpt_family="Alu"	famili famili famili famili famili famili famili famili famili famili famili famili famili famili	6	pt_fam 432 pt_fam. pt_fam. pt_fam. mpleme mpleme pt_fam. pt_fam. pt_fam. mpleme
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LPSKCEVCKYVAVELKSAFEETGKTREVIGTGYGILDOKASGVKYTKSDLRLIEVTET
ICKRLLITACTRRGPAAIDLPRACQRPLRHYTTWYTKGSRW"
439. .462
//rpt_type=tandem
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Homo sapiens, clone MGC:1220 IMAGE:2959532, mRNA, complete cds.
BC008898
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 6002306.
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Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 1422)
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Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Tissue procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
LDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Blology
http://www.systemsblology.org
http://www.systemsblology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Ketteman and Anuradha Madan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg_R.
Direct Submission
Submitted (29-MAY-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
          Med., 600 N. Wolfe Street, Meyer 2-181, Baltimore, MD 21205, USA
Location/Qualifiers
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Pred. No. 1e+02;
); Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                              194
                                                                                                                                                                                                                         /note="polyleucine rich" /codon_start=1
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                                                                                                                                                                                                                                                              /product="CTG4a"
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                                                                                                                                                           /gene="CTG4a"
388. .819
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252 c 3
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Best Local Similarity 87.5%;
Matches 21; Conservative
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LOCUS
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ACCESSION
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ORIGIN
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JOURNAL
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KEYWORDS
SOURCE
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                            FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Margolis, R.L., Abraham, M.R., Gatchell, S.B., Li, S.H., Kidwai, A.S., Breschel, T.S., Stine, O.C., Callahan, C., McInnis, M.G. and Ross, C.A. Direct Submission
Submitted (02-DEC-1996) Psychiatry, Johns Hopkins Univ. Sch. of
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 962)
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31138. .31564
/rpt_family="MRES7B"
/rpt_family="Li"
join(31640. .31733,31791. .32094)
/note="838 6 91% identity EST zb50f04.rl"
31917. .32270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="MIR"
36830, 36949
/note="GRAIL 2 excellent exon, frame 1"
                                                                                                                                                   31917. .3270
/note="90% identity EST z104c10.rl"
/db_xref="dbEST:AA009751"
32354. .32655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(37800. .37874)
/rpt_family="MER91B"
38633. .38910
7/rpt_family="Alu"
38909. .38935
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complement(32690, 32798)
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complement(32793, 32997)
/rpt_family="Li"
33000, 33296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_type=tandem
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complement(30672. .31137)
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complement(34383. .34822)
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/rpt_family="Alu"
36482. .36594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family-"L1"
35142. .35273
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Best Local Similarity
Matches 21; Conserv
  repeat_region
                                      repeat_region
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AUTHORS
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Gaps

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 9 Row: o Column: 7
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 5729791.

1. 1720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ECU04423 1720 bp mRNA linear PRI 12-JUL-2001
Homo sapiens, clone MGC:3530 IMAGE:2819660, mRNA, complete cds.
BC004423
                                                                                                                                                                           LPSKCEVCKYVAVELKSAFEETGKTKEVIGTGYGILDOKASGVKYTKSDLRLIEVTETT 
ICKRLLDYSLHKERTGSNFRKGMSETFETHUNLHVKOVKVNDIPYEEMNETGABVA 
DLKKQCDVIVJEEFEBYTEDWYRNHQEEDLTEFLCANHVLKGKDTSCLAEQWSKKGDT 
AALGGKKSKKKSSRAKAAGGRSSSSKQRKELGGLEGDPSPEEDEGIOKASPLTHSPPD
                                                                    /product="Unknown (protein for MGC:4122)"
/protein_id="AAH08961.1"
/db_xref="G1:14286300"
/tarslation="MDSMPEPASRCLLLLPLLLLLLLLPAPELGPSQAGAEENDWVR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1720)
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Submitted (12 MAR-2001) National Institutes of Health, Mammalian
Gene Collection (MCG), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
MAS Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
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                                                                                                                                                                                                                                                                                                                                                                                                                   Score 19.2; DB 9; Length 1422;
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/tissue_type="Lung, small cell carcinoma"
/clone_lib="NIH_MGC_7"
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/db_xref="taxon:9606"
/note="Vector: pOTB7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                 76.8%;
ilarity 87.5%;
Conservative (
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Best Local Similarity
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BC004423/c
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ORIGIN
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                                                                                                                                                                                                                                                                                   /translation="MOSMPEPASRCILLLPLLLLLLLPAPELGPSQAGAEENDWVR"
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LCRLLDVSLAGSTAKTGKTRSTAGMSFTETLHNLVHKGVKVVMDIPYELMNETSAEVA
DLKRQCDVIVEEFERYLEDWTRNHQEEDLTFETLGHNLVKGKDTSCILAEQWSGKKGDT
AALGGKKSKKKSSRAKAAGGRSSSKQRKELGGLEGDPSPEEDEGIQKASPLTHSPPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contact: amadan@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Ketteman and Anuradha Madan
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1422)
Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (29-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                                                                                                                                                                                            /product="Unknown (protein for MGC:1220)"
/protein_id="AAH08998.1"
/db_xref="GI:14286204"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
                           /clone="MCC:1220 IMAGE:2959532"
/tissue_type="Colon, adenocarcinoma"
/clone_lib="NIH_MGC_15"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="MGC:4122 IMAGE:2959532"
/tissue_type="Colon, adenocarcinoma"
/clone_lib="NIH_MGC_15"
/lab_host="DH10B-R"
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/db_xref="taxon:9606"
                                                                                                                                     /note="Vector: pOTB7"
          'db_xref="taxon:9606"
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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BC008961.1 GI:14286319
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/codon_start=1
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1 Similarity 87.5%;
21; Conservative (
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Best Local Similarity
Matches 21; Conserv
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BC008961/c
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ORIGIN
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.6155 of consensus"

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CDS

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The true right end of clone SC22CB-20F6 is at 18120 in this sequence. The true right end of clone SC22CB-79B4 is at 105 in this
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13677. .13721
/note="MLTIC repeat: matches 1. .45 of consensus".
13834. .14027
/note="MLTID repeat: matches 1. .204 of consensus".
14069. .14363
/note="Alux repeat: matches 1. .293 of consensus".
14443. .15245
/note="matche: GSS: Em:A0747573"
15017. .15272
/note="Alux repeat: matches 35. .290 of consensus".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10651. 11166

// Anote-"LIMC1 repeat: matches 5770. .6315 of consensus"

12417. .12852

// Anote-"MLT. repeat: matches 1. .466 of consensus"

13073. .13314
                                                                                                                                                                                                                                                                                                                         /note="AluJb repeat: matches 109. .281 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7093. .720 - records b/. .130 of consensus" //note="NIR repeat: matches 50. .180 of consensus" //772. .8079 // note="Alusx repeat: matches 1. .306 of consensus" // note="LZ repeat: matches 2396. .2750 of consensus" // note="LZ repeat: matches 2396. .2750 of consensus" // note="Maxx repeat: matches 1. .293 of consensus" // 10285. .10473
                                                                                                                                                                                                                                                                                                                                                   665. .792
/note="FLAM_C repeat: matches 1. .131 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1788. .1950
hotte="L2 repeat: matches 2539. .2740 of consensus"
1942. .1100
/note="MIR repeat: matches 48. .201 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1437. .1472
/note="L2 repeat: matches 2704. .2739 of consensus"
1758. .1950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="AllSg repeat: matches 1. .313 of consensus" 5313. .5417 /note="Min repeat: matches 45. .155 of consensus" 5507. .5629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .184 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .140 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="L1P repeat: matches 87. .130 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat: matches 1. .218 of
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                                                                                                                                                                                                                                                                                                                                                                                                        820. 1366 /
/note="L1PB1 repeat: matches 5634.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note-"uncertain number of bases"
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700te-Alusg repeat: matches 21.
13496. 13500
13590. 13667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="MIR repeat: matches 47.
1853. .5165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "MIR repeat: matches 16.
                                                                                                                                                          /organism="Homo saplens"
/db_xref="taxon:9606"
  between neighbouring submissions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0285. .10473
note="MER20 repeat: ma
0551. .10606
note="28 copies 2 mer
                                                                                                                                                                                                               /chromosome="22"
/clone="SC22CB-20F6"
/clone_lib="SC22CB"
3. .189
                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3307. .5629
/note="MIR re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 862
                                                                                    sequence.
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                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (08-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire, Cabonization (18-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire, Calo ISA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requestics: clonerequest@sanger.ac.uk
On Dec 13, 1999 this sequence version replaced gi:1695140.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequence map criteria as follows. An attempt is made to resolve all sequence map within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           numbers given in the feature table with their source databases:
Ems., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP, Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 22, constructed by the Sanger Centre Chromosome 22
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr22
SC22CB-20F6 is from the human chromosome 22-specific cosmid library
(SC22CB-20F6 is from the human chromosome 22-specific cosmid library
(SC22CB-20F6) constructed at the Sanger Centre by Mark Ross and Cordelia
                                                                                                                                                                                /translation="MOSMPEPASRCLLLLPLLLLLLLPAPELGPSQAGAEENDWVR LPSKCEVCXVVXVVVELKSAFEETGKTKEVIGTGTGILDQKASGVKTTKSDLRLIEVTET LPSKCEVCXVVVVAVVAVETRERGKTKSTESTFETLHVLKGVVVANDIPYELMNETSAEVA DLKKQCDVIVVEEFEEVIEDWYRNHQEEDLTPELCANHYLKGKDTSCLAEQWSKKGDT AALGGKKSKKKSSRAKAAGGRSSSSKQRKELGGLEGDPSPEEDEGIOKASPLTHSPPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 18120 bp DNA linear PRI 12-DEC-1999 DNA sequence from clone SC22CB-20F6 on chromosome 22,
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MDORTANT: This sequence is not the entire insert of clone SC220B-20F6 It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1720;
                                                                                            /product-"Unknown (protein for MGC:3530)"
/protein_id-"AAH04423.1"
/db_xref-"GI:13325208"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 19.2; DB 9; Length 1
Pred. No. 1.1e+02;
); Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                      314 t
                              'note="Vector: pOTB7"
                                                                                                                                                                                                                                                                                                                                                   526 g
/lab_host-"DH10B-R"
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0
                                                                                 /codon_start=1
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Whiteley, M.
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1 Similarity 87.5%;
21; Conservative
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                                                     .1224
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                                                                                                                                                                                                                                                                                                                                                      389
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Human

DEFINITION

RESULT HSB20F6

Query Match Best Local S Matches 21

ô d

BASE COUNT ORIGIN

human.

TITLE JOURNAL REFERENCE AUTHORS

COMMENT

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

.296 of consensus"

misc\_feature

Query Match

Matches

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BASE COUNT

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7540. 3520

Anote-"LibAdA repeat: matches 6197. 6277 of consensus"

4703. 4772

A1724 repeat: matches 369. 444 of consensus"
5085. 5180

Anote-"Tigger2a repeat: matches 299. 369 of consensus"
5085. 5180

Anote-"Tigger2a repeat: matches 246. 299 of consensus"
5476. 5525

Anote-"Tigger2a repeat: matches 246. 299 of consensus"
5844. 6032

Anote-"Tigger2a repeat: matches 1. .123 of consensus"
6563. 6699

Anote-"MERRIB repeat: matches 91. .157 of consensus"
7000. 7061

Anote-"MERRIB repeat: matches 91. .157 of consensus"
8465. 8599

Anote-"FLAM_C repeat: matches 1. .133 of consensus"
10905. .11215

Anote-"FLAM_C repeat: matches 1. .309 of consensus"
7006-"Alussi repeat: matches 1. .309 of consensus"
7006-"Alussi repeat: matches 1. .309 of consensus"
7006-"Alussi repeat: matches 1. .309 of consensus"
7007-"Alussi repeat: matches 1. .309 of consensus"
7008-"Alussi repeat: matches 1. .309 of consensus"
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LPSKCEVCKYVAVELKSAFEETGKTREVIGTGYGILDOKASGVKTTKSDLRLIEVTET
LPSKLCEVCKYVAVELKSAFERGKSFEFETLHULVHGGVKVWDIPYELMNETSAEVA
DLKKCLDVLVEFFERTGSNFRAGKSFEFETLHULVHGGVKVWDIPYELMNETSAEVA
AALGGKKSKKKSSRAKAAGGRSSSKORKELGGLEGDPSPEEDEGIQKASPLTHSPPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(join(12117. .12836,13197. .13314,13565. .13687,
15734. .15830,16806. .16929,21683. .22204))
/gene="dJ475N16.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="owing to a frameshift at 15781 compared to cDNA emig80744 our translation differs considerably from the published tr:015412 protein, adding two more coding exons to 3' or C-terminal end; match: proteins: Tr:015412"
                                                                                                                                                                                                     'note="MER51B repeat: matches 504. .617 of consensus"
                                                                                                                                            'note="Alu repeat: matches 1. .70 of consensus"
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/product="dJ45816.1 (CTG4A)"
/protein_id="CAB7530.1"
/db_xref="G1:6969163"
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                                                        /clone="RP3-475N16"
                                                                                   /clone_lib="RPCI-3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="dJ475N16.1"
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/chromosome="6"
/map="p12.3-21.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human DNA sequence from clone RP3-475N16 on chromosome 6p12.3-21.2. Contains the genes for CTG4A, pre-T cell receptor alpha, a novel protein similar to RP17A (60S ribosomal protein L7A) and the 3' end of gene KIAAO240. Contains ESTs, STSs, GSSs and four putative CpG islands, complete sequence. AL035SS AL035SS AL035SS GI:6002306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Emm., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORNPEP; Information on the WORNPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence assembly data is compared from overlapping clones.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.sanger.ac.uk/HGP/Chr6
RP3-475N16 is from the library RPCI-3 constructed at the Roswell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (02-FBB-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Sep 30, 1999 this sequence version replaced gi:5921383.
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                   .2710 of consensus"
                          .503 of consensus"
                                                                                                                                                                                                     .312 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                 Length 18120;
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                 /note="MLT1D repeat: matches 1. .5(
16121. .16339
16131. .1637
16133. .1657
/note="match: GSS: Em:AQ762426"
17544. .17885
17544. .17885
a 4734 c 4887 g 4694 t
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details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                              Score 19.2; DB 9;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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1. 113109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DD 11564 AGCTGAGTCGTGGACTCCATGGCC 11587
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 agctcagacatggactccatggcc 24
.16022
                                                                                                                                                                                                                                                                                                                                              76.8%;
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Williams, S.
                                                                                                                                                                                                                                                                                                                                                                                                       21; Conservative
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VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

AUTHORS TITLE

REFERENCE

JOURNAL

COMMENT

FEATURES

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DEFINITION

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RESULT 1 HS475N16

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Submitted (09-MAY-2001) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA 5 (bases 1 to 171247)
                                                                                                                                                                                                                                                                                                                             PRI 03-JAN-2002
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Submitted (19-JUN-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
3 (bases 1 to 171247)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (16-NOV-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases I to 171247)
Waterston, R.H.
The sequence of Homo saplens clone
Unpublished
        consensus"
                                                                                                                                                                                                                                                                                                              ACU07881 171247 bp DNA linear PRI 03-JAN
Homo sapiens chromosome 2 clone RP11-467P9, complete seguence.
AC007881
                                                                                                                                               Gaps
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Submitted (03-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
On Nov 16, 2000 this sequence version replaced 91:7631010.
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Center code: WUGSC
/note="LlP4 repeat: matches 5703. .5817 of 41336. .41377
/note="21 copies 2 mer ac 90% conserved" 41779. .41844
                                                                                                                                             Indels
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Pred. No. 1.2e+02;
); Mismatches 3;
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                                                                                                                                           0; Mismatches
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1. 171247
Arganism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="RP11-467P9"
46831 a 37692 c 38499 g 48225
                                                                                                                                                                                                          Db 21815 GCTCAGGCATTGAATCCATGGCC 21838
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Waterston, R.
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Waterston, R.H.
                                                                                                  Query Match 76.8%;
Best Local Similarity 87.5%;
Matches 21; Conservative
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ESTS: Em:AA913164 Em:AI263200 Em:AI285999 Em:AW014894
Em:AI767176"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /evidence=not_experimental
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/protein_id="CAB75302.1"
/db_xref="f0:669164"
/translation="MAGTWILLILLALGCPALPTGVGGTPFPSLAPPIMILVDGKQQMV
VYCLVLDVAPPGLDSPIWFSAGNGSALDAFTYGPSPATDGTWTNLAHIS.LPSEELASW
EPLYCHTGPGABGHSRSTQPMHLSGEASTARTCPQPELRGGGLLRAPERFILAGTPG
GALWICGVIRLLIFFULLITGSCLCDPAGPLSPATTTRILRALGSHRLHPATETG
GREATSSPRPQPRDRRWGDTPPGGRKPGSPVWGEGSYLSSYPTCPAQAMCSRSALRAPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="dJ4j5N16.2"
complement(join(25571. .26188,27131. .27175,28057. .28377,
35277. .35438)
/gene="dJ475N16.2"
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/note="LlMB3 repeat: matches 6024. .6137 of consensus"
38610, .38858
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/note="Alusc repeat: matches 1. .306 of consensus"
30593. .30668
/note=="LINBB repeat: matches 6101. .6170 of consens
33433. .33494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .309 of consensus"
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/evidence=not_experimental
complement(25571. .35438)
/gene="dJ475N16.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .6024 of
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                                                                                                  /note="match: STS: Em:G25145 Em:G27441"
21516. .22025
/note="CpG island"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat: matches 5711.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat: matches 2.
                                                                                                                                                          /evidence-not_experimental
21749. .21784
/note-match: STS: Em:AF021121"
complement(21753. .21788)
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complement(22138. .22473)
/note="match: GSS: Em:AQ756680"
23412. .27138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(23719, .23975)
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complement(24876, .25553)
/note="match: GSS: Em:AQ383009"
complement(25571)
                                                                                                                                                                                                                                                                                             21763. 21797

21762. 21797

/notee-match: STS: Em:267474"

/notee-match: STS: Em:609799"

/ogene-md3475N16.1"
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21759, .21794
                                     /note="match: STS: Em:G37319' complement(17091, 17133)
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0; Gaps

Indels

Length 191719;

610 others

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140189, .157395
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157496. 191719
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37719 c 37756 g 61366 t
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              misc_feature
                                                                                                                misc_feature
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ORIGIN
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                                               0;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (07-FBB-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Feb 10, 2002 this sequence version replaced gi:18491505.
                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       center project name: bM10K5

Assembly program: XGAP4; version 4.5

Chemistry: Dye-terminator Big Dye; 100% of reads

Consensus quality: 189652 bases at least Q40

Consensus quality: 190520 bases at least Q30

Consensus quality: 190528 bases at least Q20

Insert size: 191119; sum-of-contigs

Insert size: 19804; 0.5% error; agarose-fp

Quality coverage: 9.71x in Q20 bases; sum-of-contigs Quality

coverage: 10.44x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                * NOTE: This is a 'working draft' sequence. This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
                                               .;
0
                                               Indels
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
          Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 3;
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1. 191719

1. 091719

1. Organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="X"
/clone="taxon:10K5"
/clone="taxon:10K
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7.0ote=assembly_fragment:04272
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40340. .64658
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fragment_chain:1"
64759. .81283
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/note="assembly_fragment:03265
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                                                                                                                1 agctcagacatggactccatggcc 24
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May 23, 2002, 23:05:27 ; Search time 4203.75 Seconds (without alignments) 80.267 Million cell updates/sec
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Gapop 10.0 , Gapext 1.0
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em\_gss\_hum:\* em\_gss\_inv:\* em\_gss\_pln:\* em\_estro:\* em\_htc:\* gb\_est1:\* em\_esthum:\* em\_estin:\* em\_estmu:\* em\_estov:\* em\_estpl:\* gb\_est2:\* gb\_htc:\*

Post-processing: Minimum Match 0% Maximum Match 100% . Listing first 45 summaries

em\_estba:\*

EST:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	BB999BB 68899BB	BB856691 BB856691	AA048794 m148e06.r	AA002532 mg54b02.r	AI098985 uc01q04.r	BB863087 BB863087	BB857917 BB857917	BB857913 BB857913	BG062828 L0958D12-	BB853356 BB853356	BB605812 BB605812	BB661026 BB661026	BB633565 BB633565	BB637089 BB637089	BB661603 BB661603	BB652011 BB652011	BE289316 601089839
SUMMARIES	ΩI	BB666889	BB856691	AA048794	AA002532	AI098985	BB863087	BB857917	BB857913	BG062828	BB853356	BB605812	BB661026	BB633565	BB637089	BB661603	BB652011	BE289316
	DB	6	6	σ	σ	σ	0	σ	σ	10	σ	6	σ	σ	0	σ	σ	10
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e mouse tissues.
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                  sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="ovary"
/dev_stage="2 days pregnant adult"
/dev_stage="2 days pregnant adult"
/lab.ost="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
gandadagadcGGCGCCAACTCGAGTTTTTTTTTTTTTTTVN 3'], cDNA was
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BB856691 GI:17098145
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 330)
Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T.,
Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T.,
Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa ,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="RIKEN full-length enriched, 2 days pregnant adult female ovary" /sex="female"
                                                                                                                                                                                                                                                                     Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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RIKEN integrated sequence analysis (RISA) system -- 384 - format
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                                                                                                                         Computer-based methods for the mouse full-length cDNA
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Matches 25; Conservative
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Contactory for Genome Exploration Research Group, RIKEN Genomic Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanaqawa 230-0045, Japan Tel: 81-45-503-9226
Rax: 81-45-503-9226
Rax: 81-45-503-9226
Rul: http://genome-gsc.riken.go.jp,
URL: http://genome-gsc.riken.go.jp,
Carninci, P., Shibata, Y., Hayatau, N., and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi.K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Watahiki, M., Yokazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
Hayashizaki, Y., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA048794. 382 bp mRNA linear EST 09-SEP-1996 mj48e06.rl Soares mouse embryo NbME13.5 14.5 Mus musculus CDNA clone IMAGE:479362 5', mRNA sequence.
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Eukaryota, Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 382)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Askahira,S., Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y. RIKEN Encyclopedia of Mouse Full-length cDNas (Akimura,T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="RIKEN full-length enriched, B16 F10Y cells"
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91 c 127 q 64 t
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/db_xref="taxon:10090"
                                                                                                                                                                     Unpublished (2001)
Contact: Yoshihide Hayashizaki
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AA048794.1 GI:1528466
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AI098985 435 bp mRNA linear EST 20-AUG-1998 uc01904.rl Scares_mammary_gland_NbMMG Mus musculus cDNA clone IMAGE:1396758 5' similar to TR:015412 015412 CTG4A, ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington University School of MedicineP 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: mob.REGA+ET
                                                                                                                                                                                                                                          /db_xref="taxon:10090"
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Unpublished (1996)
Contact: Marra MyMouse EST Project
Washu-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Far: 314 286 1810
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/organism="Mus musculus"
/strain="C57BL/6J"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 406)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
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                                                                                                                                         Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:290106
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 344.
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                             Unpublished (1996)
Contact: Marra MyMouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                       /strain="CS7BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:479362"
/scone="IMAGE:479362"
/sex="unknown"
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/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH108"
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Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
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/organism="Mus musculus"
Waterston, R.
The WashU-HHMI Mouse EST Project
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Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T.,
Hayateu, N., Hiramoto, K., Hiracka, T., Hirozane, T., Imotani, K., Ishii,
Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T.,
Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T.,
Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K.,
Shibata, K., Shinagawa, A., Shiraki, T., Soqabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku, Akahira, S., Tanaka, T., Tomaru, A., Tayaya, T.,
Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
RIKEN Encyclopedia of Mouse Full-length CDNAS (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BB863087 RIKEN full-length enriched, Leydig cells CRL-2065 MLTC-1 CDNA Mus musculus CDNA clone G430034D12 5', mRNA sequence.
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9226
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
             This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:908474
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                                                                                                                                                                               /strain="C57BL/6J"
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/sex="male"
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High quality sequence stop: 329.
Location/Qualifiers
                                                                                                                                                                                                                                                                                       /tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
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                                                                                                                                                                 /organism="Mus musculus"
mouseest@watson.wustl.edu
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 48);
Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T., Akimura,T., Hamoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii, Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T., Y., Ito,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
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URE.:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Carninci,P., Shibata,Y., Hayatsu,N., Sudahara,Y., Shibata,Y.
M., Konno,H., Okazaki,Y., Muzamatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
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Watahiki,M., Yoneda,Y., Inoue,K., Togawa,Y., Tanaka,T., Matsuura
,S., Rawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
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/db_xref="taxon:10090"
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Contact: Yoshihide Hayashizaki
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Email: genome-reaegac.riken.go.jp,
URL:http://genome.gac.riken.go.jp,
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'M., Konno,H., Okazak,Y., Hayatsu,N., and Hayashizaki,Y.
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wagi.K., Fujiwake,S. Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
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Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
'Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
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Piao Y. Ko, N.T., Lim, M.K. and Ko, M.S.H. Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification
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/db_xref="taxon:10090"
/clone="G370047K04"
/clone="Bib="RIKBM full-length enriched, B16 F10Y cells"
/cell_type="B16 F10Y cells"
132 c 154 g 98 t
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National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
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niaEST (http://lgsun.grc.nia.nih.gov/cDNA/cDNA.html)
Plate: L0958 row: D column: 12
Seq primer: -21M13 Reverse
High quality sequence stop: 495
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(10 (11), 1757-171 (2000)

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I (basea I to 483)
I (basea I to 481)
Athmura.T., Arakawa.T., Carninci.P., Furuno.M., Hanagaki.T.,
Hayatau.N., Hiramoto.K., Hiraoka.T., Hirozane,T., Imotani.K., Ishii.
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Mutahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y. Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="RIKEN full-length enriched, B16 F10Y cells" /cell_type="B16 F10Y cells" 132 c 159 g 97 t
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/db_xref="taxon:10090"
/clone="G370047K11"
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota, Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 502)
Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T.,
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Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K.,
Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takawu-Aahira,S., Tanaka,T., Tomaru,A., Toya,T.
RIKEN Encyclopedia of Mouse Full-length cDNAS (Akimura,T., et al.
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                                                                                                                                                                                                                                                                 /clone_lib="NIA Mouse Newborn Kidney cDNA Library2 (Short
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                                                                                                                                                                                                                                                                                                                                                /tissue_type="Newborn Kidney"
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/db_xref="niaEST:L0958D12-5"
/db_xref="taxon:10090"
                                                                               /organism="Mus musculus"
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Contact: Yoshihide Hayashizaki
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/lab_host="DH10B"
location/Qualifiers
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Bukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 608)
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Upublished (2001)
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                                                                                                                                                                                    Fex: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
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Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
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/cell_type="B16 F10Y cells"
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/strain="C57BL/6J"
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URL:http://genome.gsc.riken.go.jp,
Carninci.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
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Normalization and subtraction of cap-trapper-selected cDNAs to
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Hatahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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Laboratory for Genome Exploration Research Group, RIKEN Genomic Sclences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
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Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.rlken.go.jp/) for
further details.
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/db_xref="taxon:10090"
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RIXEN integrated sequence analysis (RISA) system--384-format RIXEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1712 (2000)

Komno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
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Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.
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URL:http://genome.gsc.riken.go.jp,
Carninci.P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
'M., Konno,H., Okazaki,Y., Muramatsu,M., and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rappid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
wagi,K., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
'S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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/lab_host="DH10B"
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Fax: 81-45-503-9216
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Mus musculus
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Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases I to 625)
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Rouda
,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Salto,F., Sakai,C., Sakai,F., Sano,H., Sasaki
,D., Shibata,K., Shinayama,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
Muramatsu,M. and Hayashizaki,Y.
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                                                              Email: genome-resigns.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carnindi.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
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Normalization and subtraction of cap-trapper-selected cDNAs to
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agi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahalki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y.
contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5, GAGAGAGAGAGGGCGCAACTCGAGTTTTTTTTTTTTVN 3/], cDNA was
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BB633565 RIKEN full-length enriched, adult male spinal cord Mus musculus cDNA clone A330062B19 5', mRNA sequence.
BB633565 GI:16469989
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Unpublished (2001)
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Best Local Similarity luv...
25, Conservative
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JOURNAL
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SOURCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases I to 641)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.,
Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda
, M., Koya, S., Mateuyama, T., Miyazaki, A., Nomura, K., Ohno, M.,
Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki
, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H.,
Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,
RIKEN, Mouse ESTS (Arakawa, T., et al. 2001)
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                                                                                                                                                                                                                                                                                                                                                                                                      /note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [6].
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musculus CDNA clone A530052E13 5', mRNA sequence.
                                                                                                                                                                                                                                                      /clone_lib="RIKEN full-length enriched, adult male spinal
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001). Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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The Institute of Physical and Chemical Research (RIKEN)
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Mismatches 0; Indels
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Contact: Yoshihide Hayashizaki
                                                                                                                                Location/Qualifiers
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

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Hayashizaki,Y.
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Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

/clone\_lib="RIKEN full-length enriched, adult male aorta

and vein'

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Location/Qualifiers

e mouse tissues

FEATURES

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Email: genome-resignsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci.P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
'M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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'S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216

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/note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                       primed with a primer [5' GAGAGAGGAAGGACCATTTTTTTTTTTTTVN 3'], cDNA was
              /tissue_type="aorta and vein"
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100.0%; Score 25; DB 9; Length 641; 100.0%; Pred. No. 0.27; 1ve 0; Mismatches 0; Indels
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RESULT 1 BB661603

prepared by using trehalose thermo-activated reverse

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
I (bases 1 to 643)
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
,M., Koya,S., Mateuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Saito,R., Sakai,K., Sano,H., Sasaki
,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Savo,H., Sasaki
,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Savo,H., Nuramatsu,M. and Hayashizaki,Y.

RIKEN Mouse ESTS (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9216
EST 26-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) (10 (11), 1757-1771 (2000) (10 (11), Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encyclopedia: real-time sequence clustering for construction of a nonrecedindant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Salto, T., Kiyosawa, H., Yamanaka, I., Alzawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
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Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: genome_resignor.riken.go.jp,
URL:http://genome.go.go.jp,
URL:http://genome.go.go.jp,
Carninci.p., Shibata,Y., Hayasu.N., Sugahara,Y., Shibata,K., Itoh
Carninci.p., Shibata,Y., Haramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
penes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y.
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Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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                                  BB661603 RIKEN full-length enriched, 0 day neonate kidney Mus
musculus cDNA clone D630047M13 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"Site_1: SalI; Site_2: BamHI; cDNA library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Computer-based methods for the mouse full-length cDNA
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/dev_stage="0 day neonate"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
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/clone="D630047M13"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e mouse tissues.
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                                  DEFINITION
                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
                                                                                                           ACCESSION
                                                                                                                                      VERSION
                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
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138
            BASE COUNT
ORIGIN
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0; Gaps ; Query Match
Best Local Similarity 100.0%; Score 25; DB 9; Length 643;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 25; Conservative 0; Mismatches 0; Indels 

Search completed: May 23, 2002, 23:05:31 Job time: 7487 sec

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85.6%;
95.7%;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy At.
COMPUTER: TRW COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 744 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                               23391
31070
31180
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22464
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3180
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STATE: Massachusetts
COUNTRY: USA
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Best Local Similarity
; NAME/KEY:
; LOCATION:
US-09-163-285-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Age Sequence 1, Age Sequence 19, P. Sequence 11, Age 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/RB_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-374-493-12
US-09-374-824-12
US-09-374-824-12
US-08-923-454A-13
US-08-399-561-1
US-08-955-138-671-3
US-08-338-671-3
                                                                                                                                                                                                                                                                                                            rotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-465-380-39
US-08-466-399-39
US-08-466-399-39
US-08-634-641-39
US-09-249-471-39
US-09-249-471-39
US-09-249-471-39
US-09-249-451-39
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US-08-249-451-39
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US-08-249-461-39
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US-09-103-840A-1
US-09-150-133-12
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                                                                                                                                                                                                                                                                                 383533 seqs, 122816752 residues
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                                                                                                                                                                                                  1 tgcgattgcccagcaaatgcgaagt
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Maximum Match 100%
Listing first 45 summaries
                                                                        - nucleic search, using sw model
                                                                                                                                                                                                                                 IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Issued_Patents_NA:*
                                                                                                                                                                  US-09-696-686-46
25
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length: 2000000000
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Maximum DB seq
                                                                                                                                                                    Title:
Perfect score:
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                                                                                                                                                                                                                                    Scoring table:
                                                                        OM nucleic
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                                                                                                                                                                                                      Sequence:
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APPLICANT: Khodadoust, Mehran
APPLICANT: Khodadoust, Mehran
TITLE OF INVENTION: NOVEL MSP-5 PROTEIN AND NUCLEIC ACID MOLECULES
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHLVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 744;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/163,285
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 21.4; DB 4;
Pred. No. 0.086;
US-08-968-685A-9
US-09-31-665-3
US-09-236-645-1
US-09-236-645-1
US-09-155-804-12
US-08-165-804-12
US-08-24-32-1
US-09-24-32-1
US-09-24-32-1
US-08-34-32-1
US-08-34-32-1
US-08-60-9937-1
US-08-60-9937-1
US-08-60-993A-57
US-08-96-4
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US-08-121-057-3
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/090,398
FILING DATE: June 24, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MII-049
TELEPHONE: (617)227-7400
TELEPHONE: (617)742-4214
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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US-08-350-741-1
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Gaps
                                                                                                                                                                                          Sequence 1, Application US/09163285 . Sequence 1 TITLE OF INVENTION: NOVEL MSP-5 PROTEIN AND NUCLEIC ACID MOLECULES TITLE OF INVENTION: AND USES THEREOF NUMBER OF SEQUENCES: 4 CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: ADDRESSE: LAHIVE & COCKFIELD, LLP STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85.6%; Score 21.4; DB 4; Length 1512; 95.7%; Pred. No. 0.099; 1; Indels 0
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Patent No. 5614397
GENERAL INFORMATION:
APPLICANT: Weissman, Irving
APPLICANT: Lagasse, Eric
TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR MODULATING
TITLE OF INVENTION: APPLICANT IN HEMATOLYMPHOID CELLS
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compartible
COMPUTER: IEM PC compartible
COMPUTER: PETENT PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/163,285
FILING DATE:
CLASSIFICATION:
  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Mandragouras, Anny E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MII-049
TELEPHONE: (617)227-7400
TELEPHONE: (617)742-4214
INPORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 1512 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/090,398
FILING DATE: June 24, 1998
ATTORNEY/AGENT INFORMATION:
                                                                     97 CGCTTGCCCAGCAAATGCGAAGT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               221 CGCTTGCCCAGCAATGCGAAGT 243
                                              3 cgattgcccagcaaatgcgaagt 25
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Best Local Similarity 95.75
Matches 22; Conservative
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: CDS
; LOCATION: 125..868
US-09-163-285-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                Boston
    22;
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US-08-200-016-1
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    Matches
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                                                                                                                                                                                                                                      COPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/200,016
FILING DATE: 22-FEB-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Rea-Venter, Barbara
REGISTRATION NUMBER: 32,750
REGISTRATION NUMBER: 06037/003001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 854-5277
TELEFAX: (415) 854-6075
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENTH: 4195 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: NIXON and VANDERHYE PC
STREET: 8th FLOOR, 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65.6%; Score 16.4; D 94.4%; Pred. No. 37; tive 0; Mismatches
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
CORRESSEE: F1sh & Richardson
STREET: 2200 Sand Hill Road, Suite 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08350741
; Patent No. 5804194
; GENERAL INFORMATION:
APPLICANT: DOUGAN G.,
APPLICANT: CHARLES 1.G.,
APPLICANT: HORMAECHE C.E.,
APPLICANT: CHARLES I.S.,
TITLE OF INVENTION: LIVE VACCINES
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952,737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/350,74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 1295 CTATTGCCCAGCAAATGC 1312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 cgattgcccagcaaatgc 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 94.4
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
                                                              STREET: 2200 Sand H
CITY: Menlo Park
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
APPLICANT: Yeas R. Laroche, Laurent S. Jespers,
APPLICANT: Yannick G.J. Gensemans, Matthew Moyle,
APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 16.2; Pred. No. 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: STORAGE
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,380
FILING DATE: June 5, 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/OCKET NUMBER: 213/268
TELECOMPUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Lyon 6 Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 39, Application US/08465380 Patent No. 5863894 GENERAL INFORMATION:
                                                                                         REFERENCE/DOCKET NUMBER: 117.
TELEDAMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEFAX: (703) 816-4100
TELEFAX: 200797 NIXM UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          496 GACTGCCCAGCAGATGCCAAG 516
                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: Linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 gattgcccagcaaatgcgaag 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 64.8%;
Best Local Similarity 85.7%;
Matches 18; Conservative
                    ATTORNEY/AGENT INFORMATION: NAME: WILSON, MARY J.
                                                                                                                                                                                                                                                                LENGTH: 1980 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3
                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                              CDS
395..1822
                                                                  REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY;
; LOCATION:
US-08-463-875A-1
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39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFICANT: DOUGAN, GORDON
APPLICANT: DOUGAN, GORDON
APPLICANT: DOUGAN, GORDON
APPLICANT: CHARLES, Ian G.
APPLICANT: CHARLES, Ian G.
APPLICANT: OGNASON, Kevin S.
APPLICANT: JOHNSON, Kevin S.
APPLICANT: CHATFIELD, Steven N.
TITLE OF INVENTION: LIVE VACCINES
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON and VANDERHYE PC.
STREET: 8th FLOOR, 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUW TYPE: FLOPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN NUMBER: US/08/463,875A
FILING DATE: US/08/463,875A
PRICK APPLICATION DATE: US/03/04/63,875A
PRICK APPLICATION DATE: US/03/04/63,875A
PROC RAPPLICATION DATE: US/03/04/63,875A
PRICK APPLICATION NUMBER: US/03/04/63,875A
PROC RAPPLICATION NUMBER: US/03/04/63,875A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 16.2; D
Pred. No. 39;
0; Mismatches
            APPLICATION NUMBER: US 07/952,737
FILING DATE: 30-NOV-1992
APPLICATION NUMBER: GB 9007194.5
FILING DATE: 30-NAR-1990
APPLICATION NUMBER: PCT/GB91/00484
FILING DATE: 28-NAR-1991
ATTORNEY AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 117-158
TELECOMMUNICATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 117-158
TELECOMMUNICATION NUMBER: 31,955
REFERENCE/DOCKET NUMBER: 31,055
TELECOMMUNICATION NUMBER: 117-158
TELECOMMUNICATION 118
SEQUENCE CHARACTERISTICS:
LENGTH: 1990 base pairs
TYPE: NUCLEIC GCId
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/340,741
FILING DATE: 07-DEC-1994
FILING DATE: 30-NOV-1992
FILING DATE: 30-NOV-1992
APPLICATION NUMBER: GB 9007194.5
FILING DATE: 30-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UMBER: PCT/GB91/00484
28-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08463875A Patent No. 5980907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        496 GACTGCCCAGCAGATGCCAAG 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 85.7%;
Matches 18; Conservative
09-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 gattgcccagcaaatgcgaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: CDS
; LOCATION: 395..1822
US-08-350-741-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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Gaps
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0
                                                                                                                                                                                                                 us-08-486 399-39
; Sequence 39 Application US/08486399
; Patent No. 366543
; Patent No. 366543
; GENERAL INPOMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens, APPLICANT: Joris H.L. Mensens, Marc J. Lawwereys, APPLICANT: Yves R. Laroche, Laurent S. Jespers, APPLICANT: Yans G.J. Gansemans, Matthew Moyle, APPLICANT: Yannick G.J. Gansemans, Matthew Moyle, APPLICANT: Peter W. Bergum
TITLE OF INVENTION: PROTEIN
STREET: SO INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STATE: California
COMPTRY: US. Angeles
ZIP: 90011
COMPUTED PROTEIN
ZIP: 90011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 79.2%; Pred. No. 35;
Matches 19; Conservative 0; Mismatches 5; Indels
                                                                                         Length 361;
                                                                                                                                  5; Indels
                                                                                           Score 16; DB 2;
Pred. No. 35;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/486,399
FILING DATE: JUN 5.1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY,AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 213/270
TELEPHONE: (213) 955.0440
TELEFAX: (213) 955.0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              213/270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Necator americanus
                                                                                                                                                                             2 gcgattgcccagcaaatgcgaagt 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Coding Sequence 16...252
                                                                                              Query Match 64.0%;
Best Local Similarity 79.2%;
Matches 19; Conservative (
  Coding Sequence 16...252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic
STRANDEDNESS:
TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
US-08-486-399-39
; NAME/KEY:
; LOCATION:
US-08-486-397-39
                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                         Length 361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 39, Application US/08486397; Sequence 39, Application US/08486397; Patent No. 586542.
GENERAL INFORMATION:
FAPLICANT: George P. Vlasuk, Patric H. Stanssens, APPLICANT: Yoris H.L. Mensens, Marc J. Lauwereys, APPLICANT: Yors R. Laroche, Laurent S. Jespers, APPLICANT: Yanick G.J. Gansemans, Matthew Moyle, APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT; TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 357
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                         64.0%; Score 16; DB 2; 79.2%; Pred. No. 35; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: 50.099
MEDIUM TYPE: 50.099
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,397
FILING DATE: June 5, 1995
CLASSIFCATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/326,110
RIGHGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 213/269
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELEFA: (7-3510
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                          2 gegattgeceageaaatgegaagt 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth Street STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
ORGANISM: Necator americanus
                                                                                                                     ORIGINAL SOURCE:
ORGANISM: Necator americanus
                                                                                                                                                                           ; NAME/KEY: Coding Sequence
; LOCATION: 16...252
US-08-465-380-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 361 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
            SEQUENCE CHARACTERISTICS:
LENGTH: 361 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                 Ouery Match 64.0%
Best Local Similarity 79.2%
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                     GENERAL INFORMATION:
APPLICANT: Vlasuk, George P. Vlasuk
APPLICANT: Stanssens, Patrick Eric Hugo
APPLICANT: Bauvereys, Marc Josef
APPLICANT: Lauvereys, Marc Josef
APPLICANT: Lauvereys, Marc Josef
APPLICANT: Laroche, Yves Rene
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Gansemans, Yannick Georges Jozef
APPLICANT: Moyle, Matthew
APPLICANT: Moyle, Matthew
APPLICANT: Moyle, Matthew
APPLICANT: Moyle, Matthew
TITLE OF INVENTION: NEMATODE.EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64.0%; Score 16; DB 2;
illarity 79.2%; Pred. No. 35;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUCTWARE: WORD PERIOCE 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/634,641
FILING DATE: APTIL 19, 1996
FILING DATE: APTIL 19, 1995
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 219/136
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
Sequence 39, Application US/08634641
Patent No. 5955294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (213) 499-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 361 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 19; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE
ORGANISM: Nec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
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US-08-634-641-39
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79.2%; Pred. No. 35;
Live 0; Mismatches 5; Indels
                                                                                                                                                                                                                                 Sequence 39, Application US/08461965
Patent No. 5872098
GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
APPLICANT: Yeas R. Larche, Laurent S. Jespers,
APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: 8016 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM COmpatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,965
FILING DATE: June 5, 1995
CLASSIFICATION DATA: 9995
CLASSIFICATION DATA: 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: OCCODER 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANE L.
REFERENCE/DOCKET NUMBER: 30.158
REFERENCE/DOCKET NUMBER: 210/243
TELECOMMUNICATION INFORMATION:
TELECOMU
                    2 gcgattgcccagcaaatgcgaagt 25
                                                  74 GAGATTGTCCAGCAAATGAGGAAT 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 gcgattgcccagcaaatgcgaagt 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Coding Sequence 16...252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 79.2
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U.S.A.
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; LOCATION:
US-08-461-965-39
                                                                                                                                                                                                      US-08-461-965-39
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US-08-634-641-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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APPLICANT: Demission, received applicant: APPLICANT: Lauwereys, Marc Josef APPLICANT: Lauwereys, Marc Josef APPLICANT: Lauwereys, Marc Josef APPLICANT: Laroche, Yees Rene Harbitcant: Jespers, Laurent Stephane APPLICANT: Gansemans, Yannick Georges Jozef APPLICANT: Moyle, matthew APPLICANT: Moyle, matthew APPLICANT: Moyle, matthew APPLICANT: Bergum, Peter W. TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEIN NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth Street STREET: Suite 4700
CITY: Los Angeles STREET: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: storage COMPUTER: IBM COMPATIBLE OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                         Vlasuk, George Phillip
Stanssens, Patrick Eric Hugo
Messens, Joris Hilda Lieven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 216/270
TELECOMMUNICATION INFORMATION:
TELEPRAX: (213) 955-0440
TELERX: 67-3510
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRICE APPLICATION DATA:
APPLICATION NUMBER: 08/809,455
FILING DATE: APTil 17, 1997
APPLICATION NUMBER: PCT/USS5/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 05/1955
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/455,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
                                                                                                                  Sequence 39, Application US/09249471
Patent No. 6040441
GENERAL INFORMATION:
74 GAGATTGTCCAGCAAATGAGGAAT 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Necator americanus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Coding Sequence LOCATION: 16...252
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nucleic acid
EDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 90071
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US-09-249-471-39
                                                                           RESULT 11
US-09-249-471-39
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
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APPLICANT: Stanssens, Patrick Eric Hugo
APPLICANT: Messens, Joris Hilda Lieven
APPLICANT: Lavereys, Marc Josef
APPLICANT: Laroche, Yves Rene
APPLICANT: Laroche, Yves Rene
APPLICANT: Gansemans, Yannick Georges Jozef
APPLICANT: Moyle, Matthew
APPLICANT: Moyle, Matthew
APPLICANT: Moyle, Matthew
APPLICANT: Noyle, Matthew
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
TITLE OF EXCURNICS: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
Length 361;
                                                    5; Indels
    DB 3;
35;
                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: STOTAGE
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
SOFTWARE: WORD PEFFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/09/455
FILING DATE: APTH 17, 1997
APPLICATION NUMBER: 08/486,399
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/356,110
FILING DATE: JUNE 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: JUNE 5, 1994
ATTORNEY/AGENT INFORMATION:
  Score 16;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    216/270
                                                                                                                                                                                                                                                               Sequence 39, Application US/09249472 Patent No. 6046318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (213) 489-1600
TELEAX: (213) 955-0440
TELEX: 67-3510
SEQUENCE CHARACTERISTICS:
LENGTH: 361 base rei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                2 gcgattgcccagcaaatgcgaagt 25
                                                                                                                                             74 GAGATTGTCCAGCAAATGAGGAAT 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: BIGGS, SUZANNE L. REGISTRATION NUMBER: 30,158 REFERENCE/DOCKET NUMBER: 216
    64.0%;
llarity 79.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
       Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                US-09-249-472-39
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Query Match 64.0%; Score 16; DB 3; Length 361; Best Local Similarity 79.2%; Pred. No. 35; Matches 19; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT TITLE OF INVENTION: PROTEIN NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSE: LYON 6 LYON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lauwereys, Marc Josef
APPLICANT: Laroche, Yves Rene
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Gensemans, Yannick Georges Jozef
APPLICANT: Moyle, Matthew
APPLICANT: Bergum, Peter W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READBLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM COMPATIBLE
COMPUTER: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O8/809,455
FILING DATE: April 17, 1997
PRIOR APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/466,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/466,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/466,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Vlasuk, George Phillip
APPLICANT: Stanssens, Patrick Eric Hugo
APPLICANT: Messens, Joris Hilda Lieven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-809-455-39; Sequence 39, Application US/08809455; Patent No. 6090916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 gcgattgcccagcaaatgcgaagt 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear ORIGINAL SOURCE: ORGANISM: Necator americanus
                   TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 base pairs
TYPE: nucleic acid
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                           ) NAME/KEY: Coding Sequence;
; LOCATION: 16...252
US-09-249-451-39
                                                                                                                                                                                                   STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
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APPLICANT: Stanssens, Patrick Eric Hugo
APPLICANT: Messens, Joris Hilda Lieven
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Laroche, Yves Rene
APPLICANT: Gansemans, Yannick Georges Jozef
APPLICANT: Gansemans, Yannick Georges Jozef
APPLICANT: Myle, Matthew
APPLICANT: Myle, Matthew
APPLICANT: Brigum, Peter W.
TITLE OF INVENTION: NEWATODE-EXTRACTED SERINE PROTEASE
TITLE OF INVENTION: NEWATODE-EXTRACTED SERINE
TITLE OF INVENTION: NEWATODE.
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Layon & Lyon
STREET: 633 West Fifth Street
STREET: 631 West Fifth Street
                                                                                                                                                                                                                                                          Length 361;
                                                                                                                                                                                                                                                                                                                  5; Indels
                                                                                                                                                                                                                                                          Score 16; DB
Pred. No. 35;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: APRLI 17, 1997
APPLICATION NUMBER: PCT/U895/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/466,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: O8/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: O8/310,110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: OCCODER 18, 1994
NTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-249-451-39
; Sequence 39, Application US/09249451
; Patent No. 6087487
                                                                                                                                                                                                                                                                                                                                                                 2 gcgattgcccagcaaatgcgaagt 25
                                                                                                                                                                                                                                                                                                                                                                                                74 GAGATTGTCCAGCAAATGAGAAT 97
             TOPOLOGY: linear
ORIGINAL SOURCE:
ORGANISM: Necator americanus
                                                                                                                     NAME/KEY: Coding Sequence
LOCATION: 16...252
                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 79.2%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Vlasuk,
APPLICANT: Stansser
APPLICANT: Messens,
APPLICANT: Lauwere,
APPLICANT: Lauwere,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                          US-09-249-472-39
                                                                                              FEATURE:
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DB 3; Length 361;
35;
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Pred. No.
                                                  APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: OCCODER 18, 1994
ATTORNEY AGENT INFORMATION:
NAME: BIGGS. SUZANNE L.
RESISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
TELECHOME: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: May 24, 2002, 00:18:10 Job time: 11556 sec
    2 gcgattgcccagcaaatgcgaagt 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 GAGATTGTCCAGCAAATGAGGAAT 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
ORGANISM: Necator americanus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 64.0%;
Best Local Similarity 79.2%;
Matches 19; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coding Sequence 16...252
                                                                                                                                                                                                                                                                                                                    TELERX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 39
SEQUENCE CHARACTERISTICS:
LENGTH: 361 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                single
                   FILING DATE: June 5 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic
STRANDEDNESS:
TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY:
; LOCATION:
US-09-249-461-39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64.0%; Score 16; DB 3; Length 361; 79.2%; Pred. No. 35; tive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEMATODE-EXTRACTED SERINE PROTEASE INHIBITORS AND ANTICOAGULANT PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Stanssens, Patrick Eric Hugo
APPLICANT: Stanssens, Patrick Eric Hugo
APPLICANT: Messens, Joris Hilda Lieven
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Laroche, Yves Rene
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Moyle, Matthew
APPLICANT: Moyle, Matthew
APPLICANT: Bergum, Peter W.
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULA
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULA
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: storage
                                                      NAME: BIGGS, SUZANNE L.
REGIESTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
TELECOMMUNICATION INFORMATION:
TELEPRAX: (213) 955-0440
TELER X: 67-3510
INFORMATION FOR SEQ ID NO: 39:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM COMPATIBLE OPPRATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: WORD PERFECT 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/249,461 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/809,455
FILLING DATE: APril 17, 1997
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 39, Application US/09249461
Patent No. 6096877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 gcgattgcccagcaaatgcgaagt 25
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STREET: 633 West Fifth Street
STREET: Suite 4700
                FILING DATE: October 18, 1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                               ORGANISM: Necator americanus
                                                                                                                                                                                                                                                                                                                                                                                     Coding Sequence 16...252
                                                                                                                                                                                                                                          LENGTH: 361 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 79.23
Matches 19; Conservative
                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
APPLICATION NUMBER:
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STATE: California
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APPLICANT: Vlasuk,
APPLICANT: Stansser
APPLICANT: Messens,
APPLICANT: Lauwerey
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ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                     : NAME/KEY:
; LOCATION:
US-08-809-455-39
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Gaps .<u>`</u>

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Novel transgenic animals useful as animal model for characterization of function of a gene encoding trinucleotide repeat proteins (TRPs),
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Murthe trinucleoti
DNA sequence of an
T243 gene homologo
Human secreted exp
Human zcalc-1 DNA
Human zcalc-1 DNA
                                                                                                                                      May 24, 2002, 00:23:09 ; Search time 525.6 Seconds (without alignments) 81.664 Million cell updates/sec
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Mouse ES cell T243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.
     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                         1736436 segs, 858457221 residues
                                                                                                                                                                                                                                                                                                          25
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                                                                                               OM nucleic - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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AAS05278
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AAS05288
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25
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length: 2000000000
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Maximum DB seq
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Perfect score:
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Allen KD;

	0 ;	71.4	85.6		22	AAF93625	Umbilical vein and
	11	21.4	85.6		21	AAZ49678	Cardium
	77	21.4	85.6		22	AAF94104	Primer specific fo
		21.4	85.6		22	AAC90704	Secretory
	. \$1	21.4	85.6		20	AAZ24902	secreted n
	15	21.4	85.6		22	AAD05462	200000000000000000000000000000000000000
	16	21.4	85.6		22	AAD05464	Secreted a
	17		85.6		22	AAF93914	DOWN GOOD
	18		85.6		20	AAX78923	
	19		85.6		21	AAA16621	
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	55		85.6		22	AAS46164	DNA enco
	23		85.6		21	AA249677	
	24		85.6		20	AAX88064	zcalc-1 DNA
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י כ	<b>5</b> 0		8.7		23	ABL17251	Drosophila melanog
υ (	2 0		72.8		22	AAK94725	•
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O	0 4	7.	20 0		53	AAS50725	Staphylococcus aur
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		17	∞ (	107	23	AAS51969	
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						ALIGNMENTS	
RES	RESULT.	-					
AAS	81	4					
Ωį	0	5281	standard;	DNA;	25 BP	•	
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V X	AAS05281	5281;					
ă	07-SI	-SEP-2001	(first	st entry	_		
×							
GE:	PCR 1	primer	#2 used	ţ	amplify	T243 homologous	sednences.
XX	5		٠.				
X 3	trane	fransgeric animal. be	de repu	eat prot	e1n;		
X	frag	fragile x s	syndrome	Williat, Allockout Mouse	nate.	; tripiet repeat disease: mouse:	expansion; PCR primer: se

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contains heterozygous disruption in a gene encoding TRP
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The present sequence for PCR primer #2 is used to amplify sequences homologous to the T243 gene which encodes for a trinucleotide repeat protein (TRP). The invention describes methods of producing embryonic stem (ES) cells comprising a heterozygous disruption in a target DNA sequence (preferably gene T243) encoding a TRP and of producing a knockout mouse comprising a homozygous disruption in a gene encoding TRP, where the disruption inhibits the production of the wild type TRP. The invention also relates to identifying agents capable of affecting a phenotype of a knockout mouse. Also described are methods of determining whether expansion of the trinucleotide repeat in a gene encoding TRP produces a phenotypic change. The transgenic animals and the cells are useful for identifying compounds capable of ameliorating disease useful for identifying compounds capable of ameliorating disease. Symptoms, and as test substrates for the identification of divus, pharmaceuticals, therapies and interventions which may be effective in treating trinucleotide repeat discorders e.g. fragile X syndrome and turnington's disease. The animal models for trinucleotide repeat conserved in human disease. Using the mice, it is possible to model both and the pathogenic mechanism and the trinucleotide repeat instability in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 25 BP; 7 A; 6 C; 7 G; 5 T; 0 other;
Claim 14; Fig 13; 106pp; English.
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ó Query Match
Best Local Similarity 100.0%; Score 25; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.0048;
Matches 25; Conservative 0; Mismatches 0; Indels q δ

Mouse ES cell T243 gene PCR primer #432. AAS05288 standard; DNA; 25 BP. (first entry) 07-SEP-2001 AAS05288; AAS05288/c RESULT 

Trinucleotide repeat protein; TRP; T243; embryonic stem cell; ES; transgenic animal; knockout mouse; triplet repeat expansion; mouse; PCR primer; SS.

WO200130798-A1. Mus sp.

26-OCT-2000; 2000WO-US29382 99US-0161488 26-OCT-1999; 03-MAY-2001.

Moore M, Klein R, Matthews W, (DELT-) DELTAGEN INC.

WPI; 2001-300473/31.

Allen KD;

Novel transgenic animals useful as animal model for characterization of function of a gene encoding trinucleotide repeat proteins (TRPs), contains heterozygous disruption in a gene encoding TRP -

Example 12; Fig 13; 106pp; English

The present sequence for PCR primer #432 is used to amplify the T243

gene from an RI mouse embryonic stem cell genomic library. The T243 gene
encodes for a trinucleotide repeat protein (FFP). The invention describes

ceres a trinucleotide repeat protein (FFP). The invention describes

ceres a knockout mouse comprising a hemorygous disruption in a target DNA sequence (preferably T243) encoding a FRP and

ceres a knockout mouse comprising a hemorygous disruption in a

ceres a knockout mouse comprising a hemorygous disruption in a

ceres a phenotype of a knockout mouse. Also described are methods

confectually TRP. The invention also relates to identifying agents capable

confectually where the disruption inhibits the production of the

confectual preparation of the trinucleotide repeat in a gene

confectual preparation of the trinucleotide repeat in a gene

confectual preparation of the trinucleotide of ammiltorial

characterial are useful for identifying compounds capable of ammiltorial

confectual preparation of the trinucleotide repeat in a gene

confectual preparation of the trinucleotide repeat

confectual preparation of the trinucleotide repeat

confectual preparation of dispease in

confectual model systems to study the progression of disease in

confectual pathogenic mechanism and the trinucleotide repeat in spathity in the

conserved in human disease. Using the mice, it is possible to model both

conserved in human disease.

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Sequence 25 BP; 5 A; 7 C; 6 G; 7 T; 0 other;

Gaps ; 0 Length 25; Indels 100.0%; Score 25; DB 22; 100.0%; Pred. No. 0.0048; iive 0; Mismatches 0; Query Match 100.0 Best Local Similarity 100.0 Matches 25; Conservative

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1 tgcgattgcccagcaaatgcgaagt 25 qq δλ

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Gaps

AAS05283 standard; DNA; 49 BP RESULT AAS05283

(first entry) 07-SEP-2001 AAS05283;

Trinucleotide repeat protein; TRP; T243; embryonic stem cell; ES; transgenic animal; knockout mouse; triplet repeat expansion; fragile X syndrome; Huntington's disease; mouse; PCR primer; ss. PCR primer #489 used to amplify T243 PCR product from pool A7

Mus sp.

26-OCT-2000; 2000WO-US29382. WO200130798-A1 03-MAY-2001.

Moore M, 99US-0161488 Matthews W, (DELT-) DELTAGEN INC. 26-OCT-1999; Klein R, 

Allen KD;

Novel transgenic animals useful as animal model for characterization of function of a gene encoding trinucleotide repeat proteins (TRPs), contains heterozygous disruption in a gene encoding TRP -WPI; 2001-300473/31.

Example 12; Fig 13; 106pp; English.

The present sequence for PCR primer #489 is used to further amplify a T243 gene PCR product from pool A7 (obtained by PCR of the T243 gene

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from an R1 mouse embryonic stem cell genomic library). Gene T243 encodes for a trinucleotide repeat protein (TRP). The invention describes methods of producing embryonic stem (ES) cells comprising a heterozygous disruption in a target DNA sequence (preferably gene T243) encoding a TRP and of producing a knockout mouse comprising a homozygous disruption in a gene encoding TRP, where the disruption inhibits the production of the wild type TRP. The invention also relates to identifying agents capable of affecting a phenotype of a knockout mouse. The transgenic animals and the cells are useful for identifying compounds capable of ameliorating disease symptoms, and as test substrates for the identification of drugs, pharmaceuticals, therapies and interventions which may be effective in treating trinucleotide repeat disorders e.g. fragile X syndrome and Huntington's disease. The animal models for trinucleotide repeat disorders are ideal model systems to study the progression of diseases in vivo, the molecular basis of these diseases and show the features observed in human disease. Using the mice, it is possible to model both the pathogenic mechanism and the trinucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 25; DB 22; Length 49; 100.0%; Pred. No. 0.0054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murine trinucleotide repeat protein (TRP) cDNA sequence.
                                                                                                                                                                                                                                                                                                                                                       Sequence 49 BP; 9 A; 13 C; 14 G; 13 T; 0 other;
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                                                                                                                                                                                                                                                                                                                       repeat instability in the mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; Fig 11; 106pp; English
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/product= "TRP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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The present sequence encodes for murine trinucleotide repeat protein (TRP). The invention describes methods of producing embryonic stem (ES) cells comprising a heterozygous disruption in a target DNA sequence (preferably gene T243) encoding a TRP and of producing a knockout mouse (alsruption inhibits the production of the wild type TRP. The invention also relates to identifying agents capable of affecting a phenotype of a knockout mouse. Also described are methods of determining whether a knockout mouse. Also described are methods of determining whether a knockout mouse. Also described are methods of determining whether a knockout mouse. Also described are methods of determining whether a knockout mouse. Also described are methods of determining whether a knockout mouse of the trinucleotide repeat in a gene encoding TRP produces a phenotypic change. The transgenic animals and the cells are useful for dentifying compounds capable of amellorating disease symptoms, and as test substrates for the identification of drugs, pharmaceuticals, therapies and interventions which may be effective in treating to trinucleotide repeat disorders e.g. fraqile X syndrome and Huntington's disease. The animal models for trinucleotide repeat disorders are ideal model systems to study the progression of disease in vivo, the molecular basis of these diseases and show the features observed in human disease. Using the mice, it is possible to model both the pathogenic mechanism and the trinucleotide repeat instability in the mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 25; DB 22; Length 1839; 100.0%; Pred. No. 0.011; Live 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1839 BP; 424 A; 522 C; 535 G; 358 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         test substrates for the identification of drugs, pharmaceuticals, theraples and interventions which may be effective in treating trinuclectide repeat disorders e.g. fraqile X syndrome and Huntington's disease. The animal models for trinuclectide repeat disorders are ideal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel transgenic animals useful as animal model for characterization of function of a gene encoding trinucleotide repeat proteins (TRPs), contains heterozygous disruption in a gene encoding TRP -
                                                                                                                                                                                                                                        protein (TRP).
                                                                                                                                                              expanded T243
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                                                                                                                                                                                                                                        gene. The T243 gene encodes for a trinucleotide repeat protein (The invention describes methods of producing embryonic stem (ES)
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                                                                                                                                                              sequence represents the DNA sequence of an
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repeat protein (TRP). The invention describes methods of producing embryonic stem (ES) cells comprising a heteroxygous disruption in a target DNA sequence (perferably gene T243) encoding a TRP and of producing a knockout mouse comprising a homozygous disruption in a gene encoding TRP. where the disruption inhibits the production of the wild type TRP. The invention also relates to identifying agents capable of affecting a phenotype of a knockout mouse. Also described are methods of determining whether expansion of the trinucleotide repeat in a gene encoding TRP produces a phenotypic change. The transgenic animals and the cells are useful for identifying compounds capable of ameliorating disease symptoms, and as test substrates for the identification of drugs, pharmacouticals, therapies and interventions which may be effective in treating trinucleotide repeat disorders e.g. fragile X syndrome and Huntington's disease. The animal models for trinucleotide repeat to vivo, the molecular basis of these diseases and show the features observed in human disease. Using the mice, it is possible to model both the pathogenic mechanism and the trinucleotide repeat instability in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expressed sequence tag; EST; probe; chemotactic; proliferative; immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic; thrombolytic; antiinflammatory; cytostatic; antibacterial; antifundal; antiinflammatory; cytostatic; antiparkinsonian; antiviral; antidiabetic; antiasthmatic; vulnerary; antiparkinsonian; antiulcer; osteopathic; neuroprotective; nootropic; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cerebroprotective; anticonvulsant; antidepressant; gene therapy; vaccine, autoimmune disorder; multiple solerosis; allergic condition; insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer; lymphoid cell deficiency; burn; osteoporosis; osteoarthritis; central nervous system disorder; Alzheimer's disease; stroke; Parkinson's disease; Huntington's disease; coaqulation disorder; haemophilia; thrombosis; inflammatory disorder; Crohn's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; mouse; chicken; rat; secreted expressed sequence tag; sEST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Evans C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96.0%; Score 24; DB 22; Length 370; 100.0%; Pred. No. 0.025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Collins-Racie LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted expressed sequence tag SEQ ID NO:2104.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 370 BP; 73 A; 86 C; 149 G; 62 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tumour; infection; depression; psoriasis; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA45529 standard; cDNA; 238 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US24206.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24; Conservative
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Merberg D, Treacy M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-317938/27
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Best Local Similarity
Matches 24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200021991-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-APR-2000.
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AAA45529
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AMA ANA4326 to AAA45925 represent specifically claimed secreted expressed sequence tags (SESTs), isolated from human, mouse, chicken and rat casequence tags (SESTs), isolated from human, mouse, chicken and rat tissues they were isolated from. The activities depending on the tissues they were isolated from. The activities depending on chemotactic; proliferative; immunomodulatory; haematopoletic; chemotactic; analgeaid; haemastatic; thrombolytic; antinflammatory; cytostatic; analgeaid; antilucer; osteopathic; neuroprotective; antiasthmatic; vulnerary; antilucer; osteopathic; neuroprotective; antiasthmatic; vulnerary; antilucer; osteopathic; neuroprotective; conditionsing and in vaccines. The SESTs are useful as probes for the anticonvulsant; and antidepressant. The SESTs are useful as probes for the condition and isolation of full-length convac of the sest of the molecules which correspond to the SESTs. Proteins encoded by the SESTs of are useful in assays for determining biological activity and raising (multiple sclerosis, insulin dependent diabetes), allorations conditions (stephma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers, costeoporosis, osteoartritis, central nervous system disorders (Alzheimer's, Parkinson's, Huntington's disorders (crohn's Crostesse), tumentington's disorders (crohn's correspond to all deficiencies, wounds, burns, ulcers, costeoporosis, osteoartritis, central nervous system disorders (crohn's parkinson's, hartington's disorders (crohn's crostesse), tumentington's disease, strokey, coadulation cold sease), tumentington's disease, strokey, coadulation cold sease), tumentington's disease, tumentington's disease, the morphila, the morphila, fungal or viral infections, depression and the morphila, the morphila of the morphila, the morphila, 
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                     Isolated polynucleotides, and encoded proteins, comprising secreted expressed sequence tags (sESTs), useful for treating various disorders such as autoimmune, infectious, and central nervous system disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Calcitonin-like protein 1; zcalc-1; human; osteopathic; antidiabetic; hypotensive; vasodilator; neuromodulator; peripheral organ; treatment; Paget's disease; hypercalcaemia; osteoporosis; Raynaud's disease; type I diabetes; hypertension; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 85.6%; Score 21.4; DB 21; Length 238; Best Local Similarity 95.7%; Pred. No. 0.46; Matches 22; Conservative 0; Mismatches 1; Indels 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note- "calcitonin-like protein 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 238 BP; 51 A; 51 C; 80 G;.56 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualiflers
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                                                                                                                      Claim 1; Page 729; 803pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                155 cgcttgcccagcaaatgcgaagt 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 cgattgcccagcaaatgcgaagt 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX88062 standard; DNA; 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98WO-US26940.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human zcalc-1 DNA allele 1.
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AAX88062
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                                                                                                                                                                            This invention describes a novel human polynuclectide that encodes a calcitonin-like polypeptide which has osteopathic, antidiabetic and hypotensive activity and also acts as a vasodilator. Antibodies derived from the product of the invention can be used to isolate and purify the polypeptide sequences. The polypeptides can be used as neuromodulators in a variety of peripheral organs. They can be used in the treatment of paget's disease, hypercalcaemia, and osteoporosis. They can also be used to treat Raynaud's disease, and may be able to inhibit the progression of type I diabetes. The polypeptide sequences may be administered as vasodilators to treat hypertension.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes a novel human polynucleotide that encodes a calcitonin-like polypeptide which has osteopathic, antidiabetic and hypotensive activity and also acts as a vasodilator. Antibodies derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Calcitonin-like protein 1; zcalc-1; human; osteopathic; antidiabetic; hypotensive; vasodilator; neuromodulator; peripheral organ; treatment; Paget's disease; hypercalcaemia; osteoporosis; Raynaud's disease; type I diabetes; hypertension; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                   New mammalian nucleic acid encoding a calcitonin-like polypeptide-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New mammalian nucleic acid encoding a calcitonin-like polypeptide-1
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                                                                                                                                                                                                                                                                                                                                                                                                       DB 20; Length 371;
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                                                                                                                                                                                                                                                                                                                                                   Sequence 371 BP; 79 A; 81 C; 125 G; 86 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                 85.6%; Score 21.4; DF
95.7%; Pred. No. 0.5;
tive 0; Mismatches
                                                                                                                                                  Disclosure; Page 47-48; 55pp; English.
                                             Sheppard PO;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX88063 standard; DNA; 443 BP.
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            (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                          Moore EE, Raymond FC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Moore EE, Raymond FC,
                                                                       WPI; 1999-418753/35.
P-PSDB; AAY25418.
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Best Local Similarity
Matches 22; Conserv
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Gaps

Pred. No.

95.78;

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Sequences AAF93180 - AAF93743 represent polynucleotide sequences encoding human SRT proteins. The cDNA sequences are isolated from various different human tissue cDNA libraries. The invention relates to a method for detecting cDNA encoding an SRT protein, a vector containing cDNA encoding SRT, a host cell transformed with the vector, an isolated SRT polypeptide, and an antibody which binds to SRT. The polynucleotide production of SRT polypeptides, as a hybridisation probe to screen libraries to isolate cDNAs with sequence identity to SRT polypeptides, to map the game encoding the SRT polypeptides and analysing genetic disorders, tissue typing and disease tissue detection. The SRT polypeptides for polynucleotide sequences can be used in polymerase chain reaction,
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from the product of the invention can be used to isolate and purify the polypeptide sequences. The polypeptides can be used as neuromodulators in a variety of peripheral organs. They can be used in the treatment of paget's disease, hypercalcaemia, and osteoporosis. They can also be used to treat Raynaud's disease, and may be able to inhibit the progression of type I diabetes. The polypeptide sequences may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid molecule encoding a SRT polypeptide is useful for production of recombinant SRT polypeptides, gene mapping, diagnosing genetic disorders and for gene therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Umbilical vein endothelial cell cDNA encoding SRT protein SEQ ID 446.
                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                          ;
                                                                                                                                                                                           Length 443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; SRT; gene therapy; gene mapping; tissue typing; ss
                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 510 BP; 122 A; 114 C; 168 G; 104 T; 2 other;
                                                                                             the progression of type I diabetes. The polypeptide administered as vasodilators to treat hypertension.
                                                                                                                                       Sequence 443 BP; 113 A; 94 C; 142 G; 94 T; 0 other;
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                                                                                                                                                                                           Score 21.4; DB
Pred. No. 0.52;
); Mismatches
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                                                                                                                                                                                                                                                                                 3 cgattgcccagcaaatgcgaagt 25
                                                                                                                                                                                                                                                                                                                                                                                    BP.
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0
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95.7%;
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                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                               Best Local Similarity
Matches 22; Conserv
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Score 21.4; DB 22; Length 510;

85.68;

Query Match

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The present sequence is the coding region of myocardium secreted protein CC -5 (MSP-5) cDNA which was isolated from a cDNA library prepared from a cardiac tissue sample obtained from a biopsy of a 42 year old woman cardiac tissue sample obtained from a biopsy of a 42 year old woman cardiac tissue sample obtained from a biopsy of a 42 year old woman cardiant activities. It is highly expressed in heart, hypotensive and cardiant activities. It is highly expressed in heart, brain, placentar featlung, liver, kidney, testis, small intestine and cardiular processes, especially cardiac cellular processes, MSP-5 is used to modulate the activity of one or more proteins involved in a cardiovascular disorder, e.g. congestive heart failure or cardiomyopathy. Conditions and diseases which can be treated include hypertension, atherosclerosis, coronary artery spasm, coronary artery disease, valvular disease, arrhythmias, and cardiopathies (e.g. hypertropic, dilative, or restrictive cardiomyopathies), and disorders related to under or over cardiomyopathes).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel myocardium secreted protein-5 polynucleotides, used to modulate a
                                                                                                                                                                                                                                                                          Human; myocardium secreted protein-5; MSP-5; hypotensive; cardiant; cardiac cellular process; cardiovascular disorder; cardiomyopathy; congestive heart failure; hypertension; atherosclerosis; coronary artery disease; valvular disease; arrhythmia; ss.
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                 Indels
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                                                                                                                                                                                                                                                Human myocardium secreted protein-5 coding region.
                 1;
                   Mismatches
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67..744
/*tag= c
/label= Mature_MSP-5
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                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                             206 cgcttgcccagcaaatgcgaagt 228
                                                                                                                                                         BP.
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98US-0163285.
                                                  cgattgcccagcaaatgcgaagt
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                     Conservative
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Best Local Similarity
Matches 22; Conserv
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29-SEP-1998;
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Sequence 746 BP; 201 A; 142 C; 251 G; 149 T; 3 other;

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This lime interacts to increase across Areas 310 of the invention are primers and secretory or membrane proteins represented by the Areas 310 of Areas 317 - Are 341 of Areas 310 of Areas 317 - Are 341 of Areas 317 of Areas 318 of Areas 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primer specific for DNA encoding secretory/membrane protein SEQ ID 538.
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                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; secretory protein; membrane protein; vaccine; gene therapy;
rheumatoid arthritis; diabetes; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding secretory proteins/membrane proteins, usefu
gene therapy or as candidate target molecules in drug development
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                                                                       21; Length 744;
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Seguence 744 BP; 208 A; 143 C; 254 G; 139 T; 0 other;
                                                                     Score 21.4; DB Pred. No. 0.57; 0.57; Mismatches
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                                                                                                                                                                   3 cgattgcccagcaaatgcgaagt 25
                                                                                                                                                                                                                                                                                                                                         BP.
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11-JAN-2000; 2000JP-0118775.
02-MAY-2000; 2000JP-0183766.
                                                                     85.6%;
ilarity 95.7%;
Conservative
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                                                                                              Best Local Similarity
Matches 22; Conserv
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                                                                          Query Match
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AAB3661 to AAB36675. The proteins can have cytostatic, anti-inflammatory, haematopoletic, anti-ioogulant, immunomodulatory and hepatotropic activities, and can be used as cell migratory agents, cell proliferation- stimulants and cell differentiation-inducers. The proteins are useful in the treatment and prevention of diseases such as cancer, lung function disorder, liver function disorder, and immune diseases. AAC90716 to AAC90755 represent PCR primers which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; secretory protein; cancer; immune disease; infectious disease; lung function disorder; liver function disorder; antiinflammatory; gastrointestinal disorder; cytostatic; hematopoletic; anticoagulant; immunomodulatory; hepatotropic; cell proliferation-stimulant; cell migratory agent; cell differentiation-inducer; ss.
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                                                                        Gaps
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      Length 746;
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95.7%; Pred. No. 0.57;
ive 0; Mismatches 1;
      22;
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      Score 21.4; DB
Pred. No. 0.57;
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                                                                                                                                                                                           154 cgcttgcccagcaaatgcgaagt 176
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85.6%;
95.7%;
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P-PSDB; AAB36664.
      Query Match
Best Local Similarity
Matches 22; Conserv
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Matches 22; Conser
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                                                                                                                                                                                                                                                                                                 Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obsecolast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
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The invention relates to 95 novel genes and their fragments (nucleic acid sequences: AAZ24811-Z24907; amino acid sequences AAY41308-Y41404) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypucleotides. Specific uses are described for each of the 95 polynucleotides. Specific uses are described for each of the 95 polynucleotides.
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Kyaw H, Ebner R,
                                                                                                                                                                                                                                            Human secreted protein gene 92 clone HATAC53.
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                                                        AAZ24902 standard; DNA; 1306 BP
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98US-0078578.
98US-0078579.
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98US-0080313.
98US-0080314.
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P-PSDB; AAY41399.
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19-MAR-1998;
19-MAR-1998;
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RESULT 14
                               AAZ24902
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Sequence 1306 BP; 334 A; 291 C; 377 G; 300 T; 4 other;

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                                                                                                                                                                                                                                                    Human secreted protein-encoding gene 23 cDNA clone HNTRS57, SEQ ID NO:84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAD05389-AAD05473 represent cDNAs corresponding to 29 human secreted protein genes, and AAED1546-AAED1630 represent the proteins they encode. AAED1631-AAED1660 represent human secreted protein fragments or variants. The secreted proteins and their genes are useful for preventing,
                                                                                                                                                                                                                                                                               Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; hematopoietic disorder; limmune system disorder; albes, autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; anglogenic disorder; kidney disorder;
                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding 29 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy -
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Length 1306;
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/product= "Human secreted protein"
/note= "CDS does not include start codon"
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/product= "Mature human secreted protein"
                                                                                                                                                                                                                                                                                                                                                                                  gastrointestinal disorder; pregnancy-related disorder; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; gene therapy; binding partner identification; ss.
                                Indels
 Score 21.4; DB Pred. No. 0.63;
                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ruben SM, Komatsoulis GA, Moore PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 469; 535pp; English.
                                                                           195 cgcttgcccagcaaatgcgaagt 217
                                                                                                                                                                AAD05462 standard; cDNA; 1312 BP
                                                            3 cgattgcccagcaaatgcgaagt 25
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P-PSDB; AAE01619.
                Similarity
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 Query Match
Best Local 9
                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo
                                                                                                                                    RESULT
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treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the mamuluous of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 29 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders, e.g., Alzheimer's disease, Parkinson's disease), conditive disorders, schizophrenia, asthma, altinoiders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound seatuburn, to maintain organs before transplantation, for supporting cell suburn, to maintain organs before transplantation, for supporting cell colluture of primary tissues, to regenerate tissues, to identify their cognate ligande or binding partners, and in chemotaxis, and can be used as a food additive or preservatis, and in chemotaxis, and can be used all and provide or preservative to modify storage properties.

Antibodies specific for a protein of the invention can be used in the provider or preservative and in chemotaxis, and can be used in the provider or preservative or modify storage properties. In diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein-encoding cDNA of the invention. 8×6666666666666666666666666888

Sequence 1312 BP; 334 A; 288 C; 382 G; 304 T; 4 other;

ö Gaps ö 85.6%; Score 21.4; DB 22; Length 1312; 95.7%; Pred. No. 0.63; 11 Indels 0; Mismatches 1; Indels 0; 1; Indels Query Match Best Local Similarity 95.7<sup>3</sup> Matches 22; Conservative

3 cgattgcccagcaaatgcgaagt 25 õ g

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AR142810 Sequence
AC087444 Mus muscu
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AC087135 Mus muscu
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AC02954 Homo sap1
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AC013731 Homo sap1
AC01454 Homo sap1
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AC074220 Mus muscu
AX079202 Sequence
AX13616 Sequence
AX136616 Sequence
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BC019903 Homo sapi
AX136423 Sequence
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC010844 Drosophil
AC106252 Rattus no
AC015940 Homo sapi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
      BC013549
AF361644
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AC087144
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BC0080961
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                                                                                                            May 24, 2002, 00:12:11; Search time 3953.4 Seconds (without alignments) 132.333 Million cell updates/sec
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        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                              1797656 seqs, 10463268293 residues
                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                   1 tgcgattgcccagcaaatgcgaagt
                                                                              nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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25
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cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.N.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site:
Contect: (Dickson, Mark) mcd@paxil.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="RIKEN cDNA 1600025D17 gene"
/product="RIKEN cDNA 1600025D17 gene"
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E. Fowler Avenue, Tampa, FL 33620, USA
Location/Qualifiers
1. 1909
/organism="Mus musculus"
/db_xref="taxon:10090"
/cell_line="P19; derived from matings between C3H/He
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ROD 12-MAY-2001
                                                                                                                                                                                                                Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 25 Row: j Column: 9.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/db_xref="LocusID:72029"
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/db_xref="taxon:10090"
/clone="MGC:19340 IMAGE:422133"
/tissue type="Kidney, normal. 5 month old male mouse."
/clone=11b="NcI_CGAP_Kid14"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
91. 921
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Glozak, M.A., Li, Y., Reuille, R. and Rogers, M.B.
Direct Submission
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                                                                                                                                                                                                                                                                                                                       /t-anslation="mesmaps" |
LPSKCEVCKTVAVELKSAFEETGKTREVIDTGYGILDGKGSGYKYTKSDLRILEVTET
LPSKCEVCTVAVAELKSAFEETGKTREVIDTGYGILDGKGSGYKYTKSDLRILEVTET
ICKRLLDYSLHKERFGSGNRFAKGMSETFETLHNLVHKGVKVVMDIPYELMNETSAEVA
DLKKQCDVLVEEFEEVIEDMYRNHQEEDLTEFLCANHYLKGKDTSCLABRWSGKKGDI
ASLGGKKSKKKRSGVKGSSSGSSKQRKELGGLGEDANAEEEEGVQKASPLPHSPPDEL
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2 (bases 1 to 89855)

4 (bases 1 to 89855)

6 (bases 1 to 80855)

7 (bases 1 to 80855)

8 (bandy, Montgomery, K.T., Grills, G., Lee, E., Long, J., Pomerantz, R., Ioshikhes, I.P., Shim, C., Decker, J., Thomas, E., Perera, A., Gordon, M., Goltz, J.S. and Rucherlapati, R.

9 (birect Submission

9 (birect Submission)

9 (bandished (20-JUL-2000) Department of Molecular Genetics, Albert Einstein College of Medicine Genome Center, 1300 Morris Park Ave., Bronx, NY 10461, USA

On Apr 28, 2001 this sequence version replaced gi:11276104.
                                                                                                /ceil_type="embryonal carcinoma"
/clone_lib="24 hr retinoic acid-treated P19 cDNA (Bouillet
et al., Dev. Biol., 170, 420)"
89. .919
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Han, J., Montgomerry, K.T., Grills, G., Lee, E., Long, J., Pomerantz, R., Toshikhes, I.P., Shim, C., Decker, J., Thomas, E., Perera, A., Gordon, M., Goltz, J.S. and Kucherlapati, R.
females and male animals carrying an X chromosome derived from a feral mouse (McBurney & Rogers, Dev. Biol., 89, 503)"
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/protein_id="AAK52494.1"
/db_xref="GI:14028767"
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Chemistry: Dye-terminator Big Dye; 100%
*Consensus quality: 79355 at least Q20
*Consensus quality: 75365 at least Q30
*Consensus quality: 69022 at least Q40
Estimated insert size: agarose-FP - N/A
**Estimated insert size: 89115 - sum-of-contigs
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1 (bases 1 to 510)
Baker, K.P., Goddard, A. and Wood, W.I.
Human polypeptides and methods for the use thereof Patent; WO 0107611-A 446 01-FEB-2001; Genentech, Inc. (US)
Location/Qualifiers
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Pred. No. 3.2;
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1 (bases 1 to 744)

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Rocation/Qualifiers
   73527. .74749
/note="assembly_name:Contigl19"
/4770. .75963
/note="assembly_name:Contigl18"
75984. .77905
/note="assembly_name:Contigl17"
/7926. .79236
/note="assembly_name:Contigl16"
79257. .81332
/note="assembly_name:Contigl16"
79257. .81332
/note="assembly_name:Contigl15"
81353. .83169
/note="assembly_name:Contigl15"
813190. .84096
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AR142811
AR142811.1 GI:15104097
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/db_xref="taxon:9606"
114 c 168 g 104

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    /organism="unknown"

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Best Local Similarity 100.3
Matches 24; Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 747)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Emmanlais; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 746)
Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and
Hayashi,K.
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Pred. No. 3.4;
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Patent: JP 2001029099-A 4 06-FEB-2001;
TAKEDA CHENTCAL INDUSTRIES LTD
TAKEDA CHENTCAL INDUSTRIES LTD
PN JP 2001029090-A/4
PD 06-FEB-2001
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/db_xref="taxon:9606"
142 c 251 g 149
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BD006701.1 GI:18635072
JP 2001029090-A/4.
                     85.6%;
95.7%;
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Best Local Similarity 95.7
Matches 22; Conservative
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Homo sapiens
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Best Local Similarity
Matches 22; Conserv
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AUTHORS
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AX136423
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SOURCE
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Series: IRAK Plate: 42 Row: j Column: 23.
Location/Qualifiers
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                                                                               (C12N5/10,C12R1:91),(C12P21/08,C12R1:91),C12N15/00,A61K37/02,
                                             C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12P21/08,(C12P21/02, PC
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1413)
              A61P37/00, C07K14/47, C07K16/18, C12P21/02, G01N33/15, G01N33/50,
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Direct Submission
Direct Submission
Direct Submission
Direct Submission
Gene (19-DEC-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-25590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Web site: http://www.hgsc.bcm.tmc.edu
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing DN: Baylor College of Medicine Human Genome
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Homo sapiens, clone IMAGE:4991480, mRNA, partial cds.
BC019903.1 GI:18043798
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/organism='Homo sapiens (human)'
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/db_xref="taxon:9606"
143 c 255 g 14(
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(C12N5/00,C12R1:91)
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95.7%;
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Best Local Similarity 95.7
Matches 22; Conservative
                                 G01N33/
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PC GG1N33
PC C12R1:91),
C12R1:91),
PC C12N5
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TYLKKQCETMLEBFEDIVGDWYFHHQBQPLQNFLCEGHVLPAAETACLQETWTGKEIT
DGEEWTEGEEEQEEEEEEGGORMTKTGSHPKLDREDL"

301 c 413 g 321 t
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EEFEDDTGOWYFHHQEQPLQNFLCGHVLPAAETACLQETWTGKEITDGEBKTEGEBEE
307 c 422 g 327 t
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 1419)
Ota, T., Isogai, T., Nishikawa, T., Kawai, Y., Sugiyama, T. and
Hayashi, K.
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Patent: EP 1067182-A 345 10-JAN-2001;
Helix Research Institute (JP)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                         Score 21.4; D
Pred. No. 3.6;
/note="Vector: pcMV-SPORT6"
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Pred. No. 3.6;
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/organism="Homo saplens"
/db_xref="taxon:9606"
58. .804
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95.7%;
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Best Local Similarity 95.77
Matches 22, Conservative
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source

BASE COUNT

ORIGIN

ORGANISM

SOURCE

VERSION KEYWORDS

AUTHORS TITLE

REFERENCE

JOURNAL

FEATURES

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Waterston, R.H.
Direct Submission
Submitted (29-JUN-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens BAC clone RP11-506M12 from 7, complete sequence. AC073842. 5 GI:18095607 HTG.
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                                                                                                                                                                                                                                                                                                contig of 12773 bp in length appropriate to an incomplete to the state of 1231 bp in length gap of unknown length contig of 23863 bp in length gap of unknown length gap of unknown length contig of 48041 bp in length.
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3 (bases 1 to 132764)
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contig of 4513 bp in length
gap of unknown length
contig of 8763 bp in length
gap of unknown length
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30255 c 29682 g 33675 t 1336 others
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                                                                                unknown
of 2278
              unknown
of 1339
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of 1555
                                                                                                                                                                 contig of 1730 gap of unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
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Sulston, J.E. and Waterston, R.
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4 (bases 1 to 132764)
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95.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC087144 128185 bp DNA linear HTG 09-DEC-2000 Mus musculus clone RP23-257A7, WORKING DRAFT SEQUENCE, 14 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (09-DEC-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Ammanlai; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 128185)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Consensus quality: 120168 bases at least Q40
Consensus quality: 122360 bases at least Q30
Consensus quality: 122460 bases at least Q30
Consensus quality: 122460 bases at least Q20
Estimated insert size: 243000; agarose-fp estimation
Estimated insert size: 126885; sum-of-contigs estimation
Quality coverage: 9.25 in Q20 bases; agarose-fp estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of It contigs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                       Length 1512;
                                                                                                                                                                                                                                                                                                        Indels
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                                                                                (bases 1 to 1512)
Khodadoust, M.M.
MSP-5 nucleic acid molecules and uses therefor Patent: US 6204013-A 1 20-MAR-2001;
Location/Qualifiers
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                                                                                                                                                                                                                                                                       Score 21.4; DB 6;
Pred. No. 3.7;
                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
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AC087144.1 GI:11610870
HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                 /organism="unknown"
333 c 449 a
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   GI:15104096
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                                                                                                                                                                                                                                                                     Query Match 85.6%;
Best Local Similarity 95.7%;
Matches 22; Conservative
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REFERENCE AUTHORS

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AUTHORS

RESULT 11

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Gaps

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PRI 09-JAN-2002

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The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see the project of this sequence, see the passing the passing of the sequence of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P. Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J. J. and de Jong, P. J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:18. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute
                                                                                   Missouri 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           at base
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The clone sequenced to the left is CTB-161A2, 2000 bp overlap; the clone sequenced to the right is RP13-741A20. Actual end is at base position 132764 of RP11-506M12.
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1. .397
/note="similar to EST AA009576 (NID:91470735) ze82d10.rl"
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Submitted (09-JAN-2002) Department or Generals, missouri 6: University, 4444 Forest Park Avenue, St. Louis, Missouri 6: On Jan 9, 2002 this sequence version replaced gi:14647315.
                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: H_NH0506M12
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/db_xref="taxon:9606"
/chromosome="7"
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'note="similar
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2. .397 Anote-"similar to EST AA009577 (NID:91470736) ze82d10.s1" 462. .513

AW302599 (NID:96712279) xw07b03.x1"

to EST

(NID:910143025)"

BE729033

to EST

1. .67 /note="similar t

misc\_feature misc\_feature mlsc\_feature misc\_feature

BE666576 (NID:910027167)" BF026637 (NID:910734349)"

to EST to EST

1. .67 /note="similar /note="similar

462.

repeat\_region

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/note="similar to EST AW258515 (NID:g6631496) uq36b09.yl"
2354. .2522
/note="similar to EST BF026637 (NID:g10734349)"
2359. .2522
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/note="similar to EST AW258515 (NID:96631496) uq36b09.y1"
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/note="similar to EST AW258515 (NID:96631496) uq36b09.y1"
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/note="similar to EST H17220 (NID:9883460) ym42c05.rl"
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/note="similar to EST BE666576 (NID:g10027167)"
 572. .673
/note="similar to EST BE729033 (NID:910143025)"
                                                  (NID:910734349)"
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/note="similar to EST BE664898 (NID:910024867)"
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/note-"similar to EST BI037302 (NID:g14443928)"
/note-"similar to EST BE664898 (NID:g10024867)"
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/rpt_family="L2"
2090. .2494
2090. .2242
2090. .2242
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/note="similar to EST BE534256 (NID:99762901)"
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/note="similar to EST AV723000
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/note="similar to EST BE666576
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/note="similar to EST BF026637
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2354. .2522
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/note="similar to EST T75205
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/rpt_family="(TAAA)n"
1214. .1520
/rpt_family="Alu"
1495. .1522
/rpt_family="(GAAA)n"
                                 572. .673
/note="similar to EST
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/note="similar to EST
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/note="similar to EST
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/rpt_family="Alu"
1165. .1206
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/note="similar to
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2800. 3015
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AC092483 167854 bp DNA linear HTG 21-AUG-2001 Homo sapiens chromosome UNK clone CTD-2188L12, *** SEQUENCING IN PROGRESS ***, 44 unordered pieces.
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Submitted (10-JUL-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MMO 63108, USA
On Aug 21, 2001 this sequence version replaced gi:14647307.
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note="similar to EST AA169431 (NID:g1748398) zo84g01.rl"
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/note="similar to EST AW258515 (NID:96631496) uq36b09.y1"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              'note="similar to EST AW258515 (NID:96631496) uq36b09.yl"
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Anote-"similar to EST BE534256 (NID:99762901)"
2863. 3309
Anote-"similar to EST R54265 (NID:9816167) y974h03.rl"
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'note="similar to EST H14061 (NID:9878909) ym63a03.s2"
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Anote="similar to EST BF939888 (NID:g12357208)"

506. 3669

Anote="similar to EST BE073223 (NID:g8420006)"
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/note="similar to EST BF921437 (NID:g12317325)"
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Anote—"saintlar to EST BE534256 (NID:g9762901)"

Anote—"saintlar to EST BE64898 (NID:g10024867)"
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Center project name: H MS2188L12
Sequencing vector: M13; 92%
Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 3% of reads
Chemistry: Dye-terminator Big Dye; 97% of reads
Assembly program: Phrap; version 0.990319
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AC092483.2 GI:15217361
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Waterston, R. H.
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* NOTE: This is a 'working draft' sequence. It currently consists of 44 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Consensus quality: 115486 bases at least 040 Consensus quality: 134295 bases at least 030 Consensus quality: 146715 bases at least 020 Insert size: 157000, agarose-fp insert size: 163554; sum-of-contigs Quality coverage: 2.74 in 020 bases; sum-of-contigs Quality coverage: 2.79 in 020 bases; sum-of-contigs
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2825. 3877
// note-"assembly_name:Contig22"
3978. .5593
// note-"assembly_name:Contig23"
5694. .8414
// note-"assembly_name:Contig24"
8515. .9718
// note-"assembly_name:Contig24"
8615. .9718
// note-"assembly_name:Contig26"
12616. .14390
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12616. .14390
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17461. .19531
// note-"assembly_name:Contig28"
1761. .19531
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117 167854: contig of 6738 bp

Location/Qualifiers

1. 167884

/organism="Homo sapiens"

/db_xref="kaxon:9606"

/chromosome="UNK"
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ACO87135 209958 bp DNA 11near HTG 09-DEC-2000 Mus musculus clone RP23-147H4, WORKING DRAFT SEQUENCE, 31 unordered pleces.
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Submitted (09-DEC-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Greek, CA 94598, USA Center: Joint Genome Institute
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
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Sciurognathi; Muridae; Murinae; Mus.
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Pred. No. 21;
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Center clone name: RPCI-23_147H4
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Mammalia; Eutheria; Rodentia; Si
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DOE Joint Genome Institute.
Sequencing of Mouse
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58060 a

BASE COUNT ORIGIN

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

Margolis, R. L., Abraham, M. R., Gatchell, S. B., Li, S. H., Kidwai, A. S.,

Breschel, T. S., Stine, O. C., Callahan, C., Moïnnis, M.G. and Ross, C. A.

CDNS, with long CAG trinucleotide repeats from human brain

Hum. Genet. 100 (1), 114-122 (1997)
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Bursched (02-DEC-1996) Psychiatry, Johns Hopkins Univ. Sch. of Med., 600 N. Wolfe Street, Meyer 2-181, Baltimore, MD 21205, USA 1. .962

Location/Qualifiers

1. .962

/db_xref="taxon:9606"
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Best Local Similarity 88.0
Matches 22; Conservative
                                           Conservative
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     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

9b\_gss:\*
em\_gss\_hum:\*
em\_gss\_inv:\*
em\_gss\_pin:\*
em\_gss\_vrt:\*

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|---------------|--------|----------------|--------------------------|-----|-----------|--------------------|
| Result<br>No. | Score  | Query<br>Match | Query<br>Match Length DB | DB  | QI<br>QI  | Description        |
| 1             | 1528   | 83.1           | 1553                     | 17  | AK005532  | 100 mm on CESSO WA |
| 7             | 1345.6 | 73.2           | 1586                     | 11  | AK010702  | AKOTOTO Miss muscu |
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| 4             | 743.8  | 40.4           | 793                      | 10  | B1104487  |                    |
| 'n            | 722.2  | 39.3           | 985                      | 10  | BF785328  |                    |
| 9             | 713    | 38.8           | 737                      | 10  | BC873094  |                    |
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| 0             | 8.770  | 30.0           | 942                      | 10  | BF385997  | BF385997 602046176 |
| ,<br>יעכ      | 646.8  | 35.2           | 698                      | 10  | BI110829  | BI110829 602895470 |
| 10            | 641.8  | 34.9           | 779                      | 10  | BI688404  |                    |
| 11            | 638.2  | 34.7           | 645                      | 6   | BB498921  | - α                |
| 12            | 637.8  | 34.7           | 641                      | 6   | BB637089  |                    |
| 13            | 632.8  | 34.4           | 644                      | 6   | BB190512  | BB190512 BB190512  |
| 14            | 628.4  | 34.2           | 929                      | 10  | BI082275  | BIO02122 2100712   |
| 15            | 626.4  | 34.1           | 651                      | 6   | BB385488  | BB385480 BB305480  |
| c 16          | 626    | 34.0           | 626                      | 10  | BM232538  | BM222530 W022400   |
| 17            | 979    | 34.0           | 627                      | 6   | BB531047  | BB531047 BB531047  |

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| 620.8<br>619.6<br>618.4<br>613.6   | 608<br>608<br>607.4<br>606.8   | 605.6<br>603.2<br>599.6        | 594.2<br>591.4<br>586<br>583        | 574.6<br>573.8<br>571.4<br>568.2<br>566.2                | 553<br>547<br>545.6<br>541<br>540.6<br>537.4<br>534.8                           |
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DLKKQCDVLVBEREEVIEDWYNNHQEEDLTEFLCANHVLKGKDTSCLAERWSGKKGDI
ASLGGKKSKKKRSGVKGSSSGSSKQRKELGGLGEDANAEEEEGCVQKASPLPHSPPDEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="placenta"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
72. 902
                                                                                                                                                                                                                                   Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)
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                       the
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               4 (sites)
The RIKEN Genome Exploration Research Group Phase II Team and
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Pred. No. 3.5e-273;
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/db_xref="MGD:MGI:1904753"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Functional annotation of a full-length mouse cDNA collection

Nature 409, 685-690 (2001)

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Adachi, J., Alzawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A.,

Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C.,

Carninot, P., Fukuda, S., Fukunishi, Y., Hiraoka, T., Hori, F.,

Hume, D., Imotani, K., Ishi, Y., Itoh, M., Izawa, M., Kasukawa, T.,

Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S.,

Kuthara, C., Maksuyama, T., Miyazaki, A., Nishi, K., Nomura, K.,

Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J.,

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Schrimi, L., Shibata, Y., Shibata, Y., Shinagawa, A., Shiraki, T.,

Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,

Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I.,

Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and

Hayashizaki, Y.

Direct Submission

AL Submitted (10-Jul.-2000) Yoshihide Hayashizaki, The Institute of

Physical and Chemical Research (RIKEN), Laboratory for Genome

Exploration Research Group, RIKEN Gemonic Sciences Center (GSC),

Kingawa 230-0045, Japan (F-mail:genome-resegsc.riken.go.jp,

REX.81-75-9216)
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Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues. First strand cDNA was primed with a primer
[5' AGGAGAGAGAGAGCTTTTTTTTTTTVN 3'], cDNA was
prepared by using trehalose thermo-activated reverse transcriptase
and subsequently enriched for full-length by cap-trapper. CDNA went
through one round of normalization to Rot = 5.0 and subtraction to
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    /note="data source:SPTR, source key:Q9P0F2, evidence:ISS homolog to HSPC084 (FRAGMENT)"
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0; Mismatches 9; Indels 1;
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/clone="2410050022"
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                                                                        720 agggaagaaatccaagaagaagcgcagcggagtcaagggctcctccagtggcagcaa
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/note="Organ: mammary; Vector: pcMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert 2: Skb. Library constructed by Life Technologies, catalog # 12018-016. Investigators providing samples: Lothar Hennighausen/Priscilla Furth, NIH Reference for transgenic model: Li et al., Cell Growth and Differentiation 7, 3-11 (1996). Note: this is a NCI_CGAP Library."
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Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostom Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Murinae; Murinae; Murinae; Murinae; Murinae; Murinaed Lostentp://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth Ph.D.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium.(LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10978 row. column: 17
High quality sequence stop: 761.
                                             1415 GGAAGGCCATCACCATCATTGGAGGCTTAACCTGTCAGTTACTAGGAGGTGCTGGGAGCG
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/db_xref="taxon:10090"
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Local Similarity 99.6%; Pred. No. 3.6e-131;
hes 763; Conservative · 0; Mismatches 3; 1
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VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE JOURNAL COMMENT

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RESULT BI104487

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/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dr. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"
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/strain="CZECH II (feral)"
/db_ref="taxon:10090"
/clone="IMAGE:5035030"
/clone_lib="NCI_GGAP_Lu29"
/tissue_type="sportaneous tumor, me
/tab_host="DH10B"
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: Gappas-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Arrayaed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be http://image.lih.gov
Plate: LLAM11097 row: f column: 23
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602111557F1 NCI_CGAP_Kid14 Mus musculus CDNA clone IMAGE:4239639
                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria, Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 985)

NH-MGC http://mgc.ncl.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                        BF785328.1 GI:12090364
                                                                    5', mRNA sequence.
BF785328
789 ggaactggggg 799
          783 GGAACTGCGGG 793
                                                                                                                 Mus musculus
                                                                                                         house mouse
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TITLE
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Induse musculus

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

I (bases 1 to 737)

RS NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Opublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Gapbbs-remail.nh.gov

Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed By: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM10850 row: n column: 19

High quality sequence stop: 724.
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/db_xref="Laxon:10090"
/db_nos="IMAGE:4925778"
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Technologies. Note: this is a NOI_CGAP Library."
a 248 c 173 g 164 t
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1483 gctctgcccagccttctcccagggctaccagagtaaacaccttttggcctttcggtttg
                                                                                                                                                                                                                                                                       421 GCTCTGCCCAGCCCTTCTCCCAGGCCTACCAGAGTAAACACCTTTCGGCCTTTCGGTTTG
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BG873094.1 GI:14223634
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/note-"Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH" 265 c 210 g 174 t
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               Collection (MGC)
                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can letter //lmage.lln.gov
Phttp://lmage.lln.gov
Plate: LLAMI1044 row: e column: 02
High quality sequence stop: 707.
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1. 836
1. 836
3. Acqanism="musculus"
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/db_xref="taxon:10090"
/clone="INAGE:5005033"
/clone="INAGE:5005033"
/tlssue_type="tumor, blopsy sample"
/dev_stage="5 months"
/lab_host="DH10B"
 NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene
                                                                                                                                                                                                                                                                                                                                                                                        DB 10;
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Pred, No. 5.9e-122;
); Mismatches 31;
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602873203F1 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5005033 5',
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
1 (bases 1 to 836)
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                                    Score Pred. 1
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                                   38.8%;
98.6%;
                                 Query Match 38.8
Best Local Similarity 98.6
Matches 719; Conservative
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61 CCCCCCGGGGCTGAGGAGACCGACTGGGTGCGA-TGCCCAGCAAATGCGAAGTGTGCAAG 119
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
4 a 211 c 335 g 162 t
                                                                                                                                                                                                                                                                                                       BF385997 942 bp mRNA linear EST 27-NOV-2000 602046176F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:4195627 5',
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NIH-WGC http://mgc.nci.nih.gov/.
                                                                                            gaggettaacetgteagttactaggaggtgetgggagegeeeggggttggtttggggtaa 1699
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Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

Plate: LLAM9531 row, g column: 20

High quality sequence stop: 721.
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                                                                   Gaps
7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                           1813 ataactgtaaaaaaaaaaaaaaaaa 1839
                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                              BF385997.1 GI:11367302
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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                                                                     tatgittgctgtggagctgaagtcggcttttgaggaaacgggaaagaccaaggaagtgatt
                                   TATGTTGCTGTGGAGCTGAAGTCGGCTTTTGAGGAAACGGGAAAGACCAAGGAAGTGATT
                                                                                                                                                                                                                   aaggaggactggcagcaaccggtttgccaagggtatgtcggagacctttgagacgctg
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Plate: LLAM11072 row: k column: 18
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us-09-696-686-47.rst

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// 779
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/lab_host="DH108" and larged unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies: Investigator
providing samples: Jeffrey Green, M.D., NIH"
                               op mRNA linear EST 18-SEP-2001 musculus cDNA clone IMAGE:5356184 5',
                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 779)

NIH-MGC http://mgc.ncl.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Elone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11905 row: I column: 09
High quality sequence stop: 709.
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                               dq
                                        603316338F1 NCI_CGAP_Mam6 Mus
                               779
                                                                              BI688404.1 GI:15651033
                                                      mRNA sequence.
BI688404
                                                                                                                      Mus musculus
                                                                                                           house mouse.
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Matches 744;
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DEFINITION
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                                                                                                                                          /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Stle_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lother Hennighausen/Robin Humphreys.
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                                                                                                                                                                                                                                                              Length 698;
                                                                                                                                                                                                                                                                                        2; Indels
                                                 /strain="C57/B6"
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                                                                                                                                                                                                                                                              DB 10;
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Pred. No. 5.5e-110;
0; Mismatches 2;
                                                                                                                                                                                                            117
                                    /organism≈"Mus musculus"
ity sequence stop: 692.
Location/Qualifiers
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Best Local Similarity 99.3%;
Matches 681; Conservative
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High quality
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10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.

Computer_based methods for the mouse full-length cDNA
                                                                                                                       encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, H., Fukuda, S., Hara, A., Itch, M., Kawai, J., Shibata, K. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                           Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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llarity 99.4%; Pred. No. 2.2e-108;
Conservative 0; Mismatches 4;
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URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carinfol,P, Shibata,Y., Hayatsu,M., and Hayashizaki,Y.
Carinfol,P, Shibata,Y., Muramatsu,M., and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNas to
prepare full-length cDNa libraries for rapid discovery of new
genes. Genome Res. 10 (10) 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system-384-format
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Murianae; Mus
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                                                                                                                                                                                                                                                                                                  atggatatcccctatgag-ctgtggaacgagacctcagcagaggtggctgacctcaagaa
                                              aagaggettetggaetacageetgeacaaggagagaggactggeageaaceggtttgeeaag
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
I (basea 1 to 641)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.,
HIramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda
VA, Koyas, S., Mateuyama, T., Miyazaki, A., Nomura, K., Ohno, M.,
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D., Shibata, K., Shinaqawa, A., Shiraki, T., Soqabe, Y., Suzuki, H.,
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RIKEN Mouse ESTS (Arakawa, T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical Research (RIKEN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bB637089 RIKEN full-length enriched, adult male acrta and vein Mus BB637089 or 26-OCT-2001 musculus cDNA clone A530052E13 5', mRNA sequence. BB637089 BB637089.1 GI:16472874
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UR.:http://genome.gsc.riken.go.jp,
UR.:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,M., Sugahara,Y., Shibata,K., Itoh
'M., Konno,H., Okazaki,Y., Muramatsu,M., and Hayashizaki,Y.
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Wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Matchiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
'S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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301 GCCTCATGCTCTGCCCAGCCCTTCTCCCAGGGCTACCAGAGTAAACACCTTTTGGCCTTT 360
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3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda
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                                                                                                                                           /organism="Mus musculus"
/db_xra=1staxon.10090"
/clone=1staxon.0022E13"
/clone_1lib="RIKEN full-length enriched, adult male aorta
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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Pred. No. 2.6e-108;
0; Mismatches 2;
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/dev_stage="adult"
/lab_host="DH10B"
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Hiramoto, K., Hori, T. Shii, Y. Ito, M., Kawai, J., Konno, H., Kouda
, Hiramoto, K., Hori, T., Miyazaki, A., Nomura, K., Ohno, H., Kouda
, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M.,
Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki
, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H.,
Muramatsu, M. and Hayashizaki, Y.
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Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
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                                                                                                                                                                                                                                                                                                                                                                                                      BB190512 EXT 19-0CT-2001 BB190512 RIKEN full-length enriched, adult male spinal cord Mus musculus CDNA clone A330062B19 3', mRNA sequence.
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URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carinoi,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Carinoi,P., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapped discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
y.S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   On Jun 30, 2000 this sequence version replaced gi:8851131.

Contact: Yoshihide Hayashizaki
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
T-7.22 Suchlinc-oh, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9226
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Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
RIKEN integrated sequence analysis (RISA) system--384-format
                                                                                                          agtgtgacgtgctggtggaagagtttgaagaggtgattgaggactggtacaggaaccacc
                                                                                                                                                                                                               RIKEN Mouse ESTS (Arakawa, T., et al. 2001)
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BB190512.2 GI:16270724
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Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         house mouse.
                                                                                                                                                                                                                                                                                                                                                            RESULT 13
BB190512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
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JOURNAL
                                                                                                                548
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KEYWORDS
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                                                                                                                                                                            /note—"Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5] casdaGagaAGGATCCAAGGGTCTTTTTTTTTTTTVN 3'], cDNA was
                                                      /organism="Mus musculus"
/db_ratef="taxon:10090"
/clone="A330652B19"
/clone_lib="RIKEN full-length enriched, adult male spinal
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Division of Experimental Animal Research in Riken contributed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 caatcccagggggctggaaggccatcaccatcgtgagggcttaacctgtcagttactagg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 644;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34.4%; Score 632.8; DB 9; 99.7%; Pred. No. 2.2e-107; ive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                        150 t
                                                                                                                                       /tissue_type="spinal cord"
/dev_stage="adult"
/lab_host="DH10B"
                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                      151 g
              prepare mouse tissues
                                                                                                                           /sex="male"
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DEFINITION
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JOURNAL
COMMENT
                                                             1041
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BB385488
LOCUS
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                                                                                                                                   BIO82275 656 bp mRNA linear EST 20-JUN-2001 602877456F1 NCI_CGAP_Mam2 Mus musculus CDNA clone IMAGE:5009148 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"
                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 656)
NIH-MGC http://mgc.nci.nh.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                       Email: cgapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
Gaps
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H
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                                                                                                                                                                                                                                                                                                                                                                                              found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM1054 row: p column: 13
High quality sequence stop: 656.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="FVB/N-3"
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/clone="lib="NCI_CGAP_Mam2"
/tlssue_type="tumor, blopsy sample"
/deb_host="bH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 628.4; DB 10
Pred. No. 1.4e-106;
0; Mismatches 1;
                                               1. .656 /organism "Mus musculus"
                                                                                                                                                                                  B1082275.1 GI:14500605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34.2%;
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Matches 640; Conservative
                                                                                                                                                           mRNA sequence.
                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                           house mouse.
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                                                                                                                                   LOCUS
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ORIGIN
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TITLE
JOURNAL
COMMENT
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encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
sequencing pipeline with 384 multicapillary sequencer. Genome Res. .
10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="cerebellum"
/dev_stage="0 day neonate"
/dev_stage="0 day neonate"
/dab_nost="0 hilbs"
/nab_nost="0 hilbs"
/note="Site=1: SalI: Site_2: BamHI: cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hayashizaki,Y. Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136 GGTCCTTGTCGGATGGTAAATTCGAGAACTTCCAGGACAACTCGGGTGTGGGGACAAGG 195
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                                                                     Y. and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Indels
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/db_xref="taxon:10090"
/clone="C230039G09"
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                                                                                                              1545 tectgggteeteateageetecagagtgteeeteategatetttttgeetttgteeee
                                   caatcccaggggctggaaggccatcaccatcgtggaggcttaacctgtcagttactagg
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Search completed: May 23, 2002, 23:05:57 Job time: 7513 sec

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Sequence 3, Appll Sequence 11, Appl Sequence 208, Appl Sequence 2, Appll Sequence 1, Appll Sequence 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/09163285
Patent No. 6204013
Patent No. 6204013
GENERAL INFORMATION:
GAPPLICANT: Khodadoust, Mehran
TITLE OF INVENTION: NOVEL MSP-5 PROTEIN AND NUCLEIC ACID MOLECULES
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: A
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 744;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/09/163,285
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 160.2; DB 4;
Pred. No. 8.5e-32;
PCT-US93-03985-3
US-08-478-507-11
US-09-128-275A-11
US-08-68-136-2
US-08-68-136-2
US-08-68-136-1
US-08-340-203A-2
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US-08-452-567-2
US-08-452-427-2
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US-08-545-67-1
US-08-66-392A-1
US-08-66-392A-1
US-08-66-392A-1
US-08-66-392A-1
US-08-66-392A-1
                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/090,398
FILING DATE: June 24, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-049
TELECOMMUNICATION INFORMATION:
TELECHONE: (617)742-4214
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 744 base pairs
                   CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: CDNA
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Best Local Similarity
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                                                                                                           May 24, 2002, 00:18:10 ; Search time 121.39 Seconds (without alignments) 3721.229 Million cell updates/sec
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Sequence 14, Appl
Sequence 17, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 2, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 15, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 1
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2: /cgn2_6/ptcdate/1/lna/5B_COMB.seq:*
3: /cgn2_6/ptcdate/1/lna/6A_COMB.seq:*
4: /cgn2_6/ptcdate/1/lna/6B_COMB.seq:*
5: /cgn2_6/ptcdate/1/lna/PCTUS_COMB.seq:*
6: /cgn2_6/ptcdate/1/lna/PCTUS_COMB.seq:*
           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-770-379-20
US-08-757-669A-20
US-09-230-371A-20
US-09-007-005-17
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US-09-359-081-2
US-09-359-081-2
US-09-910-647-1
US-07-884-811-15
US-07-885-971-15
US-08-194-0888-15
US-08-194-0888-15
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US-08-006-676B-2
US-08-282-845-1
US-08-428-414A-4
PCT-US94-00324-2
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Maximum Match 100%
Listing first 45 summaries
                                                                                OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
                                                                                                                                                                                               US-09-696-686-47
1839
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Match Length
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                                                                                                           135 cacadaderacadecedaacreaeredeaecedecedrecaretereadagereeredageeree 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                         495 CATIGIGGGAGACTGGTACTICCACCATCAGGAGCAGCCCCTACAAAATITICTCTGTGA 554
                         ggctgaggagaccgactgggtgcgattgcccagcaaatgcgaagtgtgcaagtatgttgc 221
                                        GENERAL INFORMATION:
APPLICANT: Khodadoust, Mehran
TITLE OF INVENTION: NOVEL MSP-5 PROTEIN AND NUCLEIC ACID MOLECULES
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                519 ctcagcagaggtggctgacctcaagaagcagtgtgacgtgctggtggaagagtttgaaga
                                                                                   222 tgtggagctgaagtcggcttttgaggaaacgggaaagaccaaggaagtgattgacaccgg
                                                                                                                                            282 ctatggcatcctggacgggaagggctctggagtcaag---tacaccaagtcggacttacg
                                                                                                                                                                      195 GCAGGTGCTGGATACAGGCAAGAGGAAGAGACACGTGCCTTACAGCGTTTCAGAGACAAG
                                                                                                                                                                                                  gttaattgaagtcactgagaccatttgcaagaggcttctggactacagcctgcacaagga
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228;
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: LAHIVE & COCKFIELD, LLP STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/09/163,285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/090,398
FILING DATE: June 24, 1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09163285 Patent No. 6204013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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US-09-163-285-1
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                                                                                                                                                                                                                                                                                                            Length 1512;
                                                                                                                                                                                                                                                                                                            Score 160.2; DB 4;
Pred. No. 1.1e-31;
0; Mismatches 228;
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REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)727-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1512 base pairs
                                                                                                                                                                                                                                                                                                              Query Match 8.7%;
Best Local Similarity 57.3%;
Matches 310; Conservative (
                                                                                                                                                linear
                                                                                                                                              nucleic acid
                                                                                                                                                                                              MOLECULE TYPE: CDNA
                                                                                                                                                          STRANDEDNESS:
TOPOLOGY: lin
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                                                                                                                                                                                                                                 NAME/KEY:
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US-09-163-285-1
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4.1%; Score 75.2; DB 1; Length 7218;
Best Local Similarity 7.2%; Pred. No. 1e-09;
Matches 32; Conservative 241; Mismatches 169; Indels 0
                                                                                                                                                                                                      Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                    30472/114 IMMU
                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY, FAGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
TREFRERENCE/DOCKET NUMBER: 30472/114 IMML
TELECOMUNICATION INFORMATION:
TELECHONE: (703)836-9300
TELEPHONE: (703)836-9300
TELEPHONE: (703)836-9300
                 ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                       COUNTRY: USA
ZIP: 22313-0299
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELET.
TELETANS (703)000 ---
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                              FILING DATE:
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                                                                         STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ttttggcctttcggtttggttcctgggtcctcatcagcctccagagtgtcccctcatcga 1584
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                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 3.1%; Score 56.2; DB 1; Best Local Similarity 7.2%; Pred. No. 7.4e-05; Matches 31; Conservative 222; Mismatches 180;
                                                       APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
CORRESPONDENCE: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30472/114 IMMU
                                                                                                                                                                      E: Foley & Lardner
1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EP 91 114 300.6
                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/232,463 FILING DATE:
Sequence 14, Application US/08232463 Patent No. 5670367 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen:
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                           ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS: LENGTH: 7218 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                          CITY: Alexandria
                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                        ADDRESSEE:
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US-08-728-323A-1
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                                                                                                                                      cactggctctcagccttctaacactgcagcccttaatacagttccttctgttgtggtga 1764
                                                                             463 gtccacaaaggggtcaaggtggtgatggatatcccctatgagctgtggaacgagacctca 522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              643 cacgtgctgaagggaaaggacacgagttgcctagcagagcggtggtctggcaagaagggg 702
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                                                                                                                                                                                                                                                                                                          GENERAL INCORNATION:
APPLICANT: Horlick, Robert A.
APPLICANT: Damaj, Bassam B.
APPLICANT: Robbins, Alan K.
TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Genes TITLE OF INVENTION: Evaryotic Cells Stably Expressing Genes FILE REPERENCE: 0867/1D903US1
CURRENT APPLICATION NUMBER: US/09/130,114
CURRENT FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 36
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Pred. No. 7.2e-05;
); Mismatches 206;
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Patent No. 5976807
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Best Local Similarity 46.5
Matches 179; Conservative
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US-09-130-114-2/c
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                                                                                                                                                                    TITLE OF INVENTION: Immediate Barly Protein From Kaposi's TITLE OF INVENTION: Sarcoma-Associated Herpesvirus, DNA TITLE OF INVENTION: Encoding Same And Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 48.6; DB 2; Length 3
Pred. No. 0.0049;
0; Mismatches 204; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION UNDER: 28,678
REFERENCE/DOCKET NUMBER: 0575/52268/JPW/MSC/SKS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                              SUFFICIAL NUMBER: US/08/728,323A FILING DATE:
                                                                                                                                                                                                                                                                        E: Cooper & Dunham LLP
1185 Avenue of the Americas
Sequence 1, Application US/08728323A Patent No. 5948676
                                                             APPLICANT: Chang, Yuan
APPLICANT: BOhenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
                                                                                                                                                                                                                                                                                                                                                                        ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid_
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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Best Local Similarity
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                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                   New York
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; LOCATION:
US-08-728-323A-1
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STATE:
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                                                                                                                                    DB 4; Length 32207;
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                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Busso, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                  806 gggaggatgccaacgccgaggaggaggagggtgtgcagaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1: Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                    US-08-757-669A-20/c; Sequence 20, Application US/08757669A; Patent No. 6183751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 451
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20: 20: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA (genomic)
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Best Local Similarity 48.4
Matches 194; Conservative
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: New York
RY: U.S.A.
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US-08-757-669A-20
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                                             2541 AGAĞCAGGAĞĞTĞGAACAĞCAAGAĞQAĞGAĞĞAĞĞAĞĞAĞĞĞÇ-AĞĞAATTAĞAĞĞAĞĞTĞĞ 2599
                                                                                                                                                                                                                                                                            APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isldore S.
APPLICANT: Edelman, Isldore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: POLYEEPTIDES FROW KAPOSI'S SARCOMA-ASSOCIATED
TITLE OF INVENTION: HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      625
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          aagagtttgaagaggtgattgaggactggtacaggaaccaccaggaggaagacctgactg
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                                                                                                                     2600 AGGAGCAAGAGCAGGAGGAGGAGGAGGAGGAGGAG 2640
                                                                                              846
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                                                                                          gggaggatgccaacgccgaggaggaggagggtgtgcagaag
                                                                                                                                                                                                                    Sequence 20, Application US/08770379
Patent No. 5849564
GEMERAL INFORMATION:
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NAME: White, John P.
REGISTATION UNDRER: 28,678
REFERENCE/DOCKET UNDRER: 52347
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEO ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: DNA (genomic) US-08-770-379-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: New York COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS
                                                                                                                                                                                                          US-08-770-379-20/c
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Best Local S
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RESULT 10
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APPLICANT: GLANG, Yuan
APPLICANT: Bohenzky, Roy A
APPLICANT: Bohenzky, Roy A
APPLICANT: Russo, James J
APPLICANT: Bedelman, Isladore S
APPLICANT: Moore, Patrick S
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND
TITLE OF INVENTION: USES THERROF
FILE REPERBNOE: 45185-6-PCT-US
CURRENT FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: US/09/230,371A
PRIOR FILING DATE: 1997-07-22
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                                19634 AGGAGTTAGAGGAGCAGGAGCAGGAGTTAGAGGAGCAGGAGCAGGAGTTAGAGGAGCAGG 19575
                                                                                                        19574 AGCAGGAGTTAGAGGAGGAGGAGGAGTTAGAGGAGC--AGGAGCAGGAGTTAGAGGA 19517
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                                                                       aatteetetgtgeeaaceaegtgetgaagggaaaggaeaegagttgeetageagageggt 685
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                                                                                                                                                                                                                            Length 32207;
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48.4%; Pred. No. 0.012;
tive 0; Mismatches 204;
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                                                                                                                                                                                                                                                                                                      806 gggaggatgccaacgccgaggaggaggagggtgtgcagaag
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SOFTWARE: Patentin Ve
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Best Local Similarity
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GENERAL INFORMATION:
APPLICANT: SZOSTAK, Jack W.
APPLICANT: INFORMATION:
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: FUSIONS
TITLE OF INVENTION: FUSIONS
TITLE OF INVENTION FUSIONS
CURRENT APPLICATION NUMBER: US/09/007,005B
CURRENT FILING DATE: 1998-01-14
EARLIER FILING DATE: 1999-01-27
EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-11-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FASLSEQ for Windows Version 4.0
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                                                                                                                  19397 AGGAGCAAGAGCAGGAGCAGGAGCAGGAGCAGCAGGAG 19357
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5.3%; Pred. No. 0.0054;
tive 101; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Translation template FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17, Application US/09007005B Patent No. 6258558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (1)...(289)
; OTHER INFORMATION: n = A,T,C or
US-09-007-005-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: RNA
ORGANISM: Artificial Sequence
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Matches 11; Conserve
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ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
       TELEFAX: (206) 236 0205
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 319 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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US-08-282-845-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Reed, Steven
TITLE OF INVENTION: Diagnosis of Leishmaniasis
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jeffrey B. Oster
STREET: 8339 SE 57th Street
CITY: Marcer Island
STATE: Washington
CURRENT FILING DATE: 1999-02-05

EARLIER APPLICATION NUMBER: 60/035,963

EARLIER FILING DATE: 1997-01-27

EARLIER FILING DATE: 1997-01-27

EARLIER FILING DATE: 1997-11-06

EARLIER FILING DATE: 1997-11-06

EARLIER FILING DATE: 1998-01-14

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PASLESEQ for Windows Version 4.0

SENTATH: 289
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WEDIUM TYPE: FLOPPY disk
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM FOC COMPATABLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/006,676B
FILING DATE: 15-JAN-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSLER, JGFIFRY B.
REGISTRATION NUMBER: 32,585
REFERENCE/DOCKET NUMBER: REED-4
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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FEATURE:
NAME/KEY: misc_feature
CATION: (1)...(289)
OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                             TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
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US-08-006-676B-2
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1689 AGCAGATGGAGGACATGCGGCAGGCGATGGCTGGCGGCGACCCCGCGTACGTGTCTGAGC 1748
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Patent No. 5719263
GENERAL INFORMATION:
APPLICANT: Reced, Steven G.
TITLE OF INVENTION: A 230kd Antigen Present in Leishmania TITLE OF INVENTION: Species
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSE: Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Macintosh
SOFTWARE: Microsoft Word for Macintosh 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/282,845
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/006,676
FILING DATE: JANUARY 15, 1993
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                                                                                                       ; ORGANISM: Leishmania chagasi
US-08-006-676B-2
ANDLECULE TYPE: CDNA tO MRNA ORIGINAL SOURCE:
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APPLICATION NUMBER:
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Patent No. 5912166
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
TITLE OF INVENTION: LEISHMANIASIS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSE: SEED and BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                  Score 44.6; DB 1; Length 3 Pred. No. 0.051; . 0; Mismatches 174; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
34,693
---- 5004-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1929 GACGCCAGCCGCACAAGATGCAG 1951
                  REFERENCE FOR THE STATE OF TELEPHONE: (206)587-0430
TELEPHONE: (206)587-0430
TELEPHONE: (206)587-0644
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3319 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.4%;
Best Local Similarity 46.1%;
Matches 149; Conservative
                                                                                                                                                                      single
     REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                              CDS
455..3319
                                                                                                                                                                                                 MOLECULE TYPE: CDNA HYPOTHETICAL: NO
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STATE: Washington
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IMMEDIATE SOURCE:
                                                                                                                                                                    STRANDEDNESS:
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                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                NAME/KEY:
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US-08-428-414A-4
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0; Mismatches 174; Indels
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Pred. No. 0.051;
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TITLE OF INVENTION: Diagnosis of Leishmaniasis
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
COFFWARE: Microsoft Word, version 5.1a
21-APR-1995
                                                                                                                                                    210121.407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application PC/TUS9400324 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1929 GACGGCAGGCGGACAAGATGCAG 1951
                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Kadlecek, Ann T.
REGISTRATION UNDABER: 2101;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELERX: (206) 682-6031
TELEX: 3723836 SEEDANDBERRY
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: cDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.4%;
Best Local Similarity 46.1%;
Matches 149; Conservative
                                                                                                                                                                                                                                                                                               LENGTH: 3319 base pairs
TYPE: nucleic acid
                                                      FILLING DATE: 21 CLASSIFICATION:
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PRIOR APPLICATION DATA:

APPLICATION UNBER:

FILING DATE:

15-JAN-1993

ATTORNEY/AGENT INFORMATION:

NAME:

PERKING, PALTICLA Anne

REGISTRATION NUMBER: 34,693

TELECOMONICATION INFORMATION:

TELEPHONE: (206) 233-0644

INFORMATION FOR ESQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 3319 base pairs

TYPE: nucleic acid

STRANDEDNESS: alinear

TOPOLOGY: linear

MOLECULE TYPE: CDNA LOMBNA

ORGANISM: Leishmania chagasi

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
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|           |        | DB              | 22                | 22                 | 22                 | 22                | 20                 | 22                 | 22                | 21                 | 21                 |  |
|           |        | Match Length DB | 1839              | 1848               | 1675               | 1362              | 1657               | 580                | 580               | 274                | 744                |  |
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P-PSDB; AAU02498 

The present sequence encodes for murine trinucleotide repeat protein (TRP). The invention describes methods of producing embryonic stem (ES) cells comprising a heterozygous disruption in a target DNA sequence (preferably gene T243) encoding a TRP and of producing a Knockout mouse comprising a homozygous disruption in a gene encoding TRP, where the disruption inhibits the production of the wild type TRP. The invention of the wild type TRP. The invention also described are methods of determining whether can knockout mouse. Also described are methods of determining whether expansion of the trinucleotide repeat in a gene encoding TRP produces a comprision of the trinucleotide repeat in a gene encoding TRP produces a contract substrates for the identification of drugs, pharmaceuticals, therapies and interventions which may be effective in treating crimucleotide repeat disorders e.g. fragile X syndrome and Huntington's disease. The animal models for trinucleotide repeat disorders e.g. fragile X syndrome and Huntington's disease. The animal models for trinucleotide repeat disorders are ideal condel systems to study the progression of disease in vivo, the molecular basis of these diseases and show the features observed in human disease. Using the mice, it is possible to model both the pathogenic mechanism and the trinucleotide repeat instability in the mouse. Novel transgenic animals useful as animal model for characterization function of a gene encoding trinucleotide repeat proteins (TRPs), contains heterozygous disruption in a gene encoding TRP -Fig 11; 106pp; English Claim 8;

G; 358 T; 0 other; Sequence 1839 BP; 424 A; 522 C; 535

240 420 540 540 300 360 360 420 480 480 300 Gaps 09 9 aagggetetggagteaagtacaccaagteggaettaeggttaattgaagteaetggagaece aagggctctggagtcaagtacaccaagtcggacttacggttaattgaagtcactgagacc ctgetecttectgececgaagetaggecegagtecegeegggggetgaggagaeetgg gtgcgattgcccagcaaatgcgaagtgtgcaagtatgttgctgtggagctgaagtcggct gccaagggtatgtcggagacctttgagacgctgcacaacctagtccacaaaggggtcaag geceaagggtatgteggagaeetttgagaegetgeaeaaectagteeacaaaggggteaag ctgctccttcctgccccgaagctaggcccgagtcccgccgggggctgaggagaccgactgg ; 0 Length 1839; 0; Indels 22; В score 1839; I pred. No. 0; 0; Mismatches 100.0%; Best Local Similarity 100. Matches 1839; Conservative Similarity Query Match 301 61 241 241 361 421 61 121 181 361 481 481 121 181 301 421 q g g g g οy g ŏ g δ 엄 á à δ Qγ ò

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The present sequence represents the DNA sequence of an expanded T243 gene. The T243 gene encodes for a trinucleotide repeat protein (TRP). The Invention describes methods of producing embryonic stem (ES) cells comprising a heterozygous disruption in a target DNA sequence (preferably gene T243) encoding a TRP and of producing a knockout mouse comprising a homozygous disruption in a gene encoding TRP, where the disruption inhibits the production of the wild type TRP. The invention also relates to identifying agents capable of affecting a phenotype of a knockout mouse. Also described are methods of determining whether expansion of the trinucleotide repeat in a gene encoding TRP produces a phenotypic change. The transgent aminals and the calls are useful for identifying compounds capable of ameliorating disease symptoms, and as
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                                                                                              Novel transgenic animals useful as animal model for characterization function of a gene encoding trinucleotide repeat proteins (TRPs), contains heterozygous disruption in a gene encoding TRP -
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Trinucleotide repeat protein; TRP; T243; embryonic stem cell, transgenic animal; knockout mouse; triplet repeat expansion; fragile X syndrome; Huntington's disease; mouse; mutant; ds.
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trinucleotide repeat disorders e.g. fragile X syndrome and Huntington's disease. The animal models for trinucleotide repeat disorders are ideal model systems to study the progression of disease in vivo, the molecular basis of these diseases and show the features observed in human disease. Using the mice, it is possible to model both the pathogenic mechanism and the trinucleotide repeat instability in the mouse.
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us-09-696-686-47.rng

polypeptide.

CDNA sequence encoding for PRO4409

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AAS21311 standard; cDNA; 1675

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RESULT AAS21311

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(first entry)

24-OCT-2001 AAS21311;

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breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy; ss.
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A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
                                                                      mammalian; cancer; lung;
                                                                         secretory and transmembrane; PRO;
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99WO-US28551
99WO-US28564
99US-0170262
99WO-US30095
99WO-US30911
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2000WO-US03056
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2000WO-US05004
2000WO-US07377
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2000WO-US0733
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2000WO-US14941
2000WO-US15264
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2000WO-US04342.
2000WO-US04414.
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Smith V, Stewart TA, Tum
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11-FEB-2000;
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31-MAR-2000;
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monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor VIIA. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polynucleotides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy.
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Pred. No. 4.5e-169;
0; Mismatches 139; Indels 6;
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The present sequence encodes for human trinucleotide repeat protein (TRP). The invention describes methods of producing embryonic stem (ES) cells comprising a heteroxygous disruption in a target DNA sequence (preferably gene T243) encoding a TRP and of producing a knockout mouse comprising a homozygous disruption in a gene encoding TRP, where the cisruption inhibits the production of the wild type TRP. The invention also relates to identifying agents capable of affecting a phenotype of a knockout mouse. Also described are methods of determining whether a knockout mouse. Also described are methods of determining whether compounds capable of ameliorating disease symptoms, and as then trinucleotide repeat in a gene encoding TRP produces a contifying compounds capable of ameliorating disease symptoms, and as therapies and interventions which may be effective in treating control of drugs, pharmaceuticals, therapies and interventions which may be effective in treating control of a disease. The animal models for trinucleotide repeat disorders e.g. fragile X syndrome and Huntington's disease. The animal models for trinucleotide repeat disorders are ideal condel systems to study the progression of disease in vivo, the molecular model systems to study the progression of disease in vivo, the molecular the mice, it is possible to model both the pathogenic mechanism and the trinuclacities are incompanian.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel transgenic animals useful as animal model for characterization of function of a gene encoding trinucleotide repeat proteins (TRPs), contains heterozygous disruption in a gene encoding TRP -
 ES:
                                                                                                                                                                                                                                                                                                                    Trinucleotide repeat protein; TRP; T243; embryonic stem cell; transgenic animal; knockout mouse; triplet repeat expansion; fragile X syndrome; Huntington's disease; human; ss.
                                                                                                                                                                                                                                                                               Human trinucleotide repeat protein (TRP) cDNA sequence.
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                                                                                                                                                                 AAS05279 standard; cDNA; 1362
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1127
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DB 22; Length 1362;

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          Indels
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  85.1%;
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Best Local Similarity
Matches 758; Conserv
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Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; ospitity disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
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970S-0058665.
970S-0058668.
970S-005869.
970S-0058971.
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12-SEP-1997;
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02-OCT-1997;
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(HUMA-) HUMAN GENOME SCI INC

. Д Greene JM, Lafleur DW; oen SM, Shi Y, Young P Feng P, Greene CA, Ruben SM, Ferrie AM, Feng F en HS, Rosen CA, Olsen HS, Ebner R, Ni J, Brewer LA, Moore PA, GL; χn

WPI; 1999-080881/07. P-PSDB; AAW78192.

encode New isolated human genes and the secreted polypeptides they encoduseful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders

Claim 1; Page 233; 380pp; English.

This sequence represents a nucleic acid molecule which encodes a secreted human protein. The gene number, and the clone it is derived from, are detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAX04302) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 86 novel genes and their fragments (nucleic acid sequences: AAX04311-X04410; amino acid sequences AAW78126-W78225) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new

us-09-696-686-47.rng

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polypeptides in a sample or by determining the presence of mutations in the new polynuclaotides. Specific uses are described for each of the 86 polynuclaotides, based on which tissues they are most highly expressed in (see AAXO4311 for described uses).
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                                                                             Length 1657;
                                                                           24.3%; Score 446; DB 20; Length 181.1%; Pred. No. 2.1e-105; ive 2; Mismatches 117; Indels
                                              Sequence 1657 BP; 361 A; 490 C; 503 G; 297 T; 6 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human ovarian PCR-subtracted cDNA library clone #1232.
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                                                                                     Local Similarity 81.1 ses 542; Conservative
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The invention comprises compositions used for the therapy and diagnosis of ovarian cancer. The compositions comprise one or more ovarian tumour proteins, their associated polynuclectides, or immunogenic portions of the proteins. The ovarian tumour polynuclectides and polypeptides are useful for stimulating and/or expanding T cells specific for a tumour protein. They are also useful for inhibiting the development of cancer in a patient with an ovarian tumour DNA or protein by incubating isolated T-cells allowing them to proliferate, and administering to the patient. The sequences can be used as markers for cancer, for example, to monitor ovarian cancer progression. Probes and primers are useful in nucleic acid hybridisation, in detecting the presence of complementary sequences in a given sample, for preparing mutant species and for preparing other genetic constructions. Sequences AAS23820-AAS25231 and AAS25328-AAS25549
                                                                                                                                                                                                                                                                                                 cancer
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                                                                                                                                                                                                                                                                     New polynucleotides encoding ovarian tumour proteins, useful for treating ovarian cancer, and as probes, primers, and markers of c progression .
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Pred. No. 7.6e-97;
0; Mismatches 49; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                represent human ovarian tumour protein cDNA clones.
                                                                                                                                                                                                                                                                                                                                           Example 1; page 301-302; 378pp; English
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90.0%;
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28-MAR-2000; 2000US-0192745.
                                                                                                                  05-FEB-2001; 2001WO-US03733
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Matches 441; Conservative
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                                                                                                                                                                                         (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                 WPI; 2001-488879/53
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                                                       WO200157207-A2
 primer; probe
                             Homo sapiens.
                                                                                     09-AUG-2001
                                                                                                                                                                                                                       Algate PA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH82377 to AAH83878 represent human ovarian tumour-associated polynucleotide sequences which encode ovarian tumour proteins. The ovarian tumour protein and polynucleotide sequences have cytostatic activity, and can be used in gene therapy and vaccine production. The ovarian tumour proteins and polynucleotides can be used to inhibit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the development of cancer, particularly ovarian cancer. They can also be used to diagnose the onset and progression of cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tumour; ovarian cancer; diagnosis; gene therapy
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Human; mouse; xenopus; rat; secreted expressed sequence tag; sEST; expressed sequence tag; EST; probe; chemotactic; proliferative: immunomodulatory; haematacpoietic; chemotactic; analgesic; haemostatic; thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal; antiviral; antidiabetic; antiasthmatic; vulnerary; antiparkinsonian; antiuleer; osteopathic; neuroprotective; nootropic; antipsoriatic; cerebroprotective; anticonvulsant; antidepressant; gene therapy; vaccine; autoimmune disorder; multiple sclerosis; allergic condition; insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer; lymphoid cell deficiency; burn; osteoporosis; osteoarthritis; central nervous system disorder; Alzheimer's disease; stroke; Parkinson's disease; Huntington's disease; coagulation disorder; haemophilia; thrombosis; inflammatory disorder; Crohn's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated polynucleotides, and encoded proteins, comprising secreted expressed sequence tags (sESTs), useful for treating various disorders such as autoimmune, infectious, and central nervous system disorders -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human secreted expressed sequence tag SEQ ID NO:1519.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tumour; infection; depression; psoriasis; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 479; 618pp; English.
                                                                                                                                                                                                                                                                                                                                                                        AAA42779 standard; cDNA; 274 BP.
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Treacy M;
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cytostatic; antibacterial; antifungal; antiviral; antidiabetic; antibacterial; antifungal; antiviral; antidiabetic; antibacterial; antifungal; antiviral; antidiabetic; antibacterial; antifungal; antidiabetic; antisathmatic; vulnerary; antifulcer; osteopathic; neuroprotective; cootropic; antiparkinsonian; antipacriatic; cerebroprotective; anticonvulsant; and antidepressant. The SESTs can be used for gene therapy and in vaccines. The SESTs are useful as probes for the content of isolation of full-length cDNAs and genomic DNA contents which correspond to the SESTs. Proteins encoded by the SESTs are useful in assays for determining biological activity and raising antibodies. They may be useful for treatment of autoimmune disorders antibodies. They may be useful for treatment of autoimmune disorders (multiple sclerosis, insulin dependent diabetes), allergic conditions cateoporosis, osteoarthritis, central nervous system disorders (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation disorders (haemophilat, thrombosis), inflammatory disorders (conditions) depression and disorders (baenophilat) fungal or viral infections, depression and psoriasis. AAA43420 to AAA43425 represent linker variants which are given to the exemplification of the present invention.
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sequence tags (SESTs), isolated from human, mouse, xenopus and rat tissue sources. The SESTs can have a range of activities depending on the tissues they were isolated from. The activities include: ofhemotactic; proliferative; immunoomodulatory; haematopoletic; chemokinetic; analgesic; haemostatic; thrombolytic; antiinflammatory;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cardiac cellular process; cardiovascular disorder; cardiomyopathy; congestive heart failure; hypertension; atherosclerosis; coronary artery disease; valvular disease; arrhythmia; ss.
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0; Mismatches 21; Indels
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Local Similarity 91.9%;
nes 237; Conservative
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The present sequence is the coding region of myocardium secreted protein 5 (MSP-5) cDNA which was isolated from a cDNA library prepared from a cardiac tissue sample obtained from a biopsy of a 42 year old woman suffering from congestive heart failure. The MSP-5 protein has hypotensive and cardiant activities. It is highly expressed in heart, print, pracents, small intestine and pituitary gland. The present sequence is used to modulate a variety of cellular processes, especially cardiac cellular processes. MSP-5 is used co modulate the activity of one or more proteins involved in a cardionyascular disorder, e.g. congestive heart failure or cardiomyopathy. Conditions and diseases which can be treated include hypertension,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        atherosclerosis, coronary artery spasm, coronary artery disease, valvular disease, arrhythmias, and cardiopathies (e.g. hypertropic, dilative, or restrictive cardiomyopathies), and disorders related to under or over
                                                                                                                                                                                                                                                                                                                                                                                Novel myocardium secreted protein-5 polynucleotides, used to modulate a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75 ggaggaggacgatgacacagaacgcttgcccagcaaatgcgaagtgtgtaagctgctgag 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gctggaagaggccttagagaatttatgtgagcggatcctggactatagtgttcacgctga 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gaggactggcagcaaccggtttgccaagggtatgtcggagacctttgagacgctgcacaa 458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.7%; Score 160.2; DB 21;
57.3%; Pred. No. 1.8e-31;
tive 0; Mismatches 228;
              /*tag= b
67..744
/*tag= c
/label= Mature_MSP-5
                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Pages 92-93; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                  variety of cellular processes
                                                                                                                                                                                                                                                           (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                         98US-0163285.
                                                                                                                                                                                                         98US-0090398
                                                                                                                                                                       99WO-US13937
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Matches 310; Conservat
                                                                                                                                                                                                                                                                                                                            WPI; 2000-136983/12
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                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAY44629
                                                                                                                                                                                                                                                                                             Khodadoust MM;
                                                                                                    409967385-A1
                                                                                                                                                                                                         23-JUN-1998;
                                                                                                                                                                                                                       29-SEP-1998;
sig_peptide
                                  mat_peptide
                                                                                                                                      29-DEC-1999
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which encode human secretory or membrane proteins represented by this introduction interacts. A MAR 19310

AARB8817 - AARB8419. Included in the invention are primers

AARB8817 - AARB8419. Included in the invention are primers

AARB8817 - AARB8419. Included in the invention are primers

AARB8817 - AARB8419. Included in the invention are primers

CDNA sequences of the invention. The invention also includes methods for the production of antibodies directed against the proteins, and cDNA

Sequences, which can be used in vaccines. The polynucleotide sequences

can be used in gene therapy. The polynucleotide sequences and the proteins they encode may be used in the prevention, treatment and alaquences associated with inappropriate secretory

proteins may also be used as DNA probes in diagnostic assays

cequences may also be used as DNA probes in diagnostic assays

cequences may also be used as DNA probes in diagnostic assays

cequences may also be used as DNA probes in samples. They may also be used to similar nucleic acid sequences in samples. They may also be used to study the expression and function of secretory proteins/membrane configurations and their role in metabolism. The polypeptides may be used as antigens in the production of antibodies against them and in assays to identify modulators (agonists and antagonists) of expression and activity. The antibodies and antagonists may also be used as therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Primer specific for DNA encoding secretory/membrane protein SEQ ID 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding secretory proteins/membrane proteins, useful in
                                     cagogtggaggtcacatacctcaagaagcagtgtgagaccatgttggaggagtttgaaga 494
                                                                                                             554
                                                                                                                                                                      This invention relates to nucleic acid sequences AAF93744 - AAF93916
                                                                                               Α;
 ctcagcagaggtggctgacctcaagaagcagtgtgacgtgctggtggaagagtttgaaga
                                                                          639 caaccacgtgctgaagggaaaggacacgagttgcctagcagagcggtggtctggcaagaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; secretory protein; membrane protein; vaccine; gene therapy; rheumatoid arthritis; diabetes; PCR primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kawai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ota T, Isogai T, Nishikawa T,
                                                                                                                                                                                                                                                                                                                                                            AAF94104 standard; DNA; 746 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-JUL-1999; 99JP-0194179.
11-JAN-2000; 2000JP-0118775.
02-MAY-2000; 2000JP-0183766.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-JUL-2000; 2000EP-0114090
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agents to down regulate expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of the polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA). Examples of diseases which may be treated include rheumatoid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, secretory protein; cancer; immune disease; infectious disease; lung function disorder; liver function disorder; antinflammatory; gastrointestinal disorder; cytostatic; haematopoietic; anticoagulant; immunomodulatory; hepatotropic; cell proliferation-stimulant; cell migratory agent; cell differentiation-inducer; ss.
                                                                                                                                                                                              ggctgaggagaccgactgggtgcgattgcccagcaaatgcgaagtgtgcaagtatgttgc 221
                                                                                                                                                                                                                                                        281
                                                                                                                                                                                                                                                                                      251
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                                                                                                                                                                                                              cctagtgcagaagggggtgaaggtggatctggggatccctctggagctttgggatgagcc 491
                                                                                                                                                                                                                                                                                                                  282 ctatggcatcctggacgggaagggctctggagtcaag---tacaccaagtcggacttacg
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                                                                                                                                                                                                                                                                                                                                                                              gttaattgaagtcactgagaccatttgcaagaggcttctggactacagcctgcacaagga
                                                                                                                                                                                                                                                                                                                                                                                            372 gcgcaagggctcactgagatatgccaagggtcagagtcagaccatggcaacactgaaagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          222 tgtggagctgaagtcggcttttgaggaaacgggaaaggaccaaggaagtgattgacaccgg
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ض
                                                                                                                                 Length 746;
                                                                                                                                                               0; Mismatches 228; Indels
                                                                                       Sequence 746 BP; 201 A; 142 C; 251 G; 149 T; 3 other;
                                                                                                                                 DB 22;
                                                                                                                                Score 160.2; DB 2
Pred. No. 1.8e-31;
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                                                                                                                                8.78;
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                                                                                                                                                                 Matches 310; Conservative
                                                         arthritis and diabetes.
                                                                                                                                                   Best Local Similarity
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                                                                                                                                   Query Match
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Sequence 1419 BP; 363 A; 307 C; 422 G; 327 T; 0 other;
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Best Local Similarity
                                                                              RESULT
                                                                                                                          q
                                                                                                                                                                                                                                                                                                     AAB3661 to AAB36675. The proteins can have cytostatic, anti-inflammatory, hemmes atopoletic, anti-rogaliant, immunomodulatory and hepatotropic activities, and can be used as cell migratory agents, cell proliferation-stimulants and cell differentiation-inducers. The proteins are useful in the treatment and prevention of diseases such as cancer, lung function disorder, liver function disorder, gastrointestinal disorder and immune diseases. AAC90116 to AAC90755 represent PCR primers which are used in the exemplification of the present invention.
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                                                                                                                                                                                                 Novel secretory protein and its salt with e.g. anti-cancer, anti-inflammatory and hematopoietic, effects, applicable as drugs in remedies and preventives to treat diseases like cancer and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75 ggaggaggacgatgacacagaacgettgeceagcaaatgegaagtgtgtaagetgetgag 134
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Pred. No. 1.8e-31;
0; Mismatches 228; Indels
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                                                                                                                          Oq1 K;
                                                                                                                       Tanaka H, Ohkubo S,
                                                                                                                                                                                                                                                                         Example 4; Page 99; 122pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 57.3%;
Matches 310; Conservative
                           19-MAY-2000; 2000WO-JP03221.
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                                                                                                                       Mog1 S,
                                                                                                                                                                     P-PSDB; AAB36664.
                                                           20-MAY-1999;
30-NOV-2000.
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g õ q õ q õ a ò g ò g ò g ò 8

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which encode human secretory or membrane proteins represented by this interaction related to the invention are primers.

AAR98317 - AAR98419. Included in the invention are primers

AAR98317 - AAR94295 and AAF6232 - AAF62318 which are used to isolate the coba sequences of the invention. The invention also includes methods for the production of antibodies directed against the proteins, and cDNA sequences, which can be used in vaccines. The polynucleotide sequences can be used in gene therapy. The polynucleotide sequences and the proteins they encode may be used in the prevention, treatment and flagnosis of diseases associated with inappropriate secretory proteins any also be used as DNA probes in diagnostic assays

CC (e.g. polymerase chain reactions (PCR) to detect and quantitate the presence of similar nucleic acid sequences in samples. They may also be used to study the expression and function of secretory proteins/membrane collypetides and function of secretory proteins/membrane collypetides and antagonism. The polypetides may be used as antigens in the production of antibodies against them and in assays to identify modulators (agonists and antagonists) of expression and antagonists may also be used as therapeutic agents to down regulate expression and activity. The antibodies and antagonists may also be used as therapeutic agents to down regulate expression and activity. The antibodies and antagonists may also be used as therapeutic agents for detecting the presence of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding secretory proteins/membrane proteins, useful gene therapy or as candidate target molecules in drug development -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human cDNA encoding a membrane or secretory protein clone PSEC0237.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; secretory protein; membrane protein; vaccine; gene therapy; rheumatoid arthritis; diabetes; ss.
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11-JAN-2000; 2000JP-0118775.
02-MAY-2000; 2000JP-0183766.
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P-PSDB; AAB88487
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22; Length 1419;

Score 160.2; DB 2; Pred. No. 2.3e-31;

8.78;

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Query Match
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228;
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This invention describes a novel human polynucleotide that encodes a calcitonin-like polypeptide which has osteopathic, antidiabetic and hypotensive activity and also acts as a vasodilator. Antibodies derived from the product of the invention can be used to isolate and purify the polypeptide sequences. The polypeptides can be used as neuromodulators in a variety of peripheral organs. They can be used in the treatment of Paget's disease, hypercalcaemia, and osteoporosis. They can also be used to treat Raynaud's disease, and may be able to inhibit the progression of type I diabetes. The polypeptide sequences may be administered as vasodilators to treat hypertension.
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                                                                                                                                                                                             New mammalian nucleic acid encoding a calcitonin-like polypeptide-1
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57.3%; Pred. No. 2.4e-31;
iive 0; Mismatches 228;
                                                                                                                                                                                                                                                 Disclosure; Page 50-52; 55pp; English.
                                                      PO;
                                                      Sheppard
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                                                   Raymond FC,
ZYMOGENETICS
                                                                                                          1999-418753/35
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Matches 310; Conserv
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AAA16618 to AAA16697 encode the human secreted proteins given in AAY94898 to AAY94890, isolated from human adult brain, adult thyroid, adult retina, feetal carcinoma, adult blood, adult neural, feetal kidney, adult placenta, adult testis, whole embryo, adult cartilage, kidney, cotal brain, adult thymus, foetal placenta, adult uterus, adult tumour, and adult bladder, cDNA libraries. The polynucleotides and proteins are predicted to have bloiogical activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals. The polynucleotides can be used as markers for tissues in which the protein is preferentially expressed, as molecular weight markers on Southern gels, and as chromosome markers or tags to identify chromosomes or to map gene positions. The proteins can be used in the treatment of immune deficiencies and disorders, such as severe combined immunedeficiency (SCID), as well as viral, bacterial, fungal and other infections. These infections include human immunodeficiency virus (HIV), hepatitis, herpesviruses, mycobacteria, Leismania spp., malaria and candidasis: The proteins so an be used to treat autolimmune disorders such as connective tissue disease, multiple sclerosis, systemic lupus erythematosis, rheumatoid arthritis, autolimmune pulmonary inflammation, cullialn-Barre syndrome, autoimmune thyroiditis, insulin dependent
                                                                                                                                                                                antibacterial; antifungal; cytostatic; antiinflammatory; dermatological; antidabetic; antiasthmatic; antiarthritic; antirheumatic; protozoacide; antithyrold; immune deficiency; severe combined immunedeficiency; SCID; infection; HIV; hepatitis; malaria; autoimmune disorder; systemic lupus; connective tissue disease; multiple sclerosis; erythematosis; rheumatoid arthritis; autoimmune pulmonary inflammation; asthma; guillain-Barre syndrome; autoimmune thyroiditis; myasthenia gravis; insulin dependent diabetes mellitus; graft-versus-host-disease; autoimmune inflammatory eye disease; allergy; ss.
                                                                                                                                                                 Human; secreted protein; immunestimulant; immunesuppressant; virucide;
                                                                                                                         Human secreted protein clone pj193_5 nucleotide sequence SEQ ID NO:7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotides encoding secreted proteins, which may have e.g. untritional, chemokine, immune stimulating or suppressing, hematopolesis regulating, tissue growth, activin/inhibin antiinflammatory or tumor inhibition activity
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Steininger RJ, Spaulding
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Merberg D, Treacy M, Agostino MJ,
Wong GG, Clark HF, Fechtel K;
  BP
AAA16621 standard; cDNA; 1462
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98US-0096815.
98US-009529.
99US-011534.
99US-011534.
99US-0115931.
99US-0132020.
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                                          AAA16621;
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Secreted protein; transmembrane protein; PRO1484; PRO4334; PRO1122; PRO1889; PRO1890; PRO1887; PRO4185; PRO4353; PRO4357; PRO4405; PRO4356; PRO41852; PRO4380; PRO4364; PRO4404; PRO4425; PRO4422; PRO4422; PRO4422; PRO4424; PRO4422; PRO4424; PRO4422; PRO4426; PRO4426; PRO4426; PRO4426; PRO4430; PRO4499; tumour; obesity; diabetes; insulinemia; kidney disorder; Bergers disease; nephropathy; Schonlein-Henoch purpura; cellac disease; dermatitis herpetiformis;
diabetes mellitus, myasthenia gravis, graft-versus-host-disease and autolimmune inflammatorry eye disease. The proteins can also be used to treat allergic conditions, such asthma. AAA16698 to AAA16774 represent probes for the human secreted proteins from the present invention.
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                                                                                                                                                 Score 160.2; DB 21; Length
Pred. No. 2.4e-31;
); Mismatches 228; Indels
                                                                                             Sequence 1462 BP; 384 A; 316 C; 431 G; 331 T; 0 other;
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Matches 310; Conserv
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222 tgtggagctgaagtcggcttttgaggaaacgggaaagaccaaggaagtgattgacaccgg

302 gcaggtgctggatacaggcaagagaagagacacgtgccttacagcgtttcagagacaag gttaattgaagtcactgagaccatttgcaagaggcttctggactacagcctgcacaagga

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422 gcgcaagggctcactgagatatgccaagggtcagagtcagaccatggcaacactgaaagg

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602 cattgtgggagactggtacttccaccatcaggagcagcccctacaaaattttctctgtga

362 gctggaagaggccttagagaatttatgtgagcggatcctggactatagtgttcacgctga 421

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The present sequence encodes a secreted or transmembrane polypeptide.
The specification describes polypeptides designated PRO1484, PRO4334,
PRO4352, PRO1899, PRO1890, PRO1895, PRO4353, PRO4455, PRO4405,
PRO456, PRO4522, PRO4480, PRO4499, PRO4452, PRO4405,
PRO6030, PRO4424, PRO4422, PRO4430 and PRO4499. PRO1889 polypeptide is
useful for diagnosing tumour in a mammal. The polypeptides, their
agonists and antagonists are useful treating a condition associated with
expression or activity of the polypeptide. Conditions treated include
obesity, diabetes or hyper-or hypo-insulinemia. The polypeptides are
capable of inducing proliferation of mammalian kidney mesangial cells
and are therefore useful for treating kidney disorders associated with
decreased mesangial cell function such as Bergers disease or other
nephropathies associated with Schonlein-Henoch purpura, celiac disease,
c dermatitis herpetiformis or Crohns disease. The nucleic acids may be used
to generate transgenic animals for use in development and screening of
therapeutically useful reagents and also for chromosome identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pan J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel secreted and transmembrane polypeptides useful for diagnosing tumour in a mammal, for identifying agonists and antagonists of the polypeptide and for therapeutic use
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                            /*tag= a
/transl_except= (pos: 423..425, aa: Lys)
108..170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eaton DL, Goddard A,
Watanabe CK, Wood WI,
Socation/Qualifiers
108..854
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P-PSDB; AAB18922.
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Stewart TA,
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 Key
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3; Gaps

DB 21; Length 1470;

Score 160.2; DB 21; Length Pred. No. 2.4e-31; 0; Mismatches 228; Indels

Query Match 8.7%; Best Local Similarity 57.3%; Matches 310; Conservative

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Search completed: May 24, 2002, 00:23:41
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BC008898 Homo sapi BC008961 Homo sapi BC004423 Homo sapi U80744 Homo sapien AX198865 Sequence AX209392 Sequence

Homo sapi Homo sapi Mus muscu Sequence

Title: Perfect score: Sequence:

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Minimum DB Maximum DB

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1882 bp mRNA linear ROD 07-SEP-2001
Mus musculus, RIKEN CDNA 1600025D17 gene, clone MGC:19340
BC013549.1 GI:15488835
MGC:
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Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1882)
Strausberg, R.
Direct Submission
Submitted (04-SEP-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC Project URL: http://mgc.nc1.nih.gov
Contact: MGC help desk
Emall: cgapbs-rémail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
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AUTHORS
TITLE
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Description

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Result

AC100626 Mus muscu AC103455 Rattus no AC084828 Mus muscu AL583866 Mouse DNA AL603802 Mus muscu E32986 Gene encodi AC107493 Rattus no AF091216 Mus muscu

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LPSRCEVCKYVAVELKSAFEETGKTKEVIDDGYGILDGKGSGVKTTKSDLRLIEVTET
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DLKKQCDVLVBEFEETJEDWY THOGEDLTFELCANHVLGKDTSCLAERWSGKKGDI
ASLGGKKSKKKRSGVKGSSSGSSKORKELGGLGEDANAEEEEGVQKASPLPHSPP
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cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
CNA Stanford University School of Medicine, Stanford, CA 943
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
                                                                                            information can be for http://image.llnl.gov
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                                                                                                                                          /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                      Score 1829.4;
Pred. No. 0;
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91. .921
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Lpskcevckvvveiksapeetgktrevidtscyglidgkgsgvkytksdlrievtet
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                                                                                                                                                                                                                                                                                                                                                                       Unpublished
2 (bases 1 to 1909)
2 (bases 1 to 1909)
Glozak, M.A. Li, Y., Reuille, R. and Rogers, M.B.
Glozak, M.A. Li, Y., Reuille, R. and Rogers, M.B.
Submitted (15-MAR-2001) Biology, University of South Florida, 4202
E. Fowler Avenue, Tampa, FL 33620, USA
                                                                                                                                                                                                                                                                                                   Mus musculus Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1909)
Glozak,M.A., Li,Y., Reuille,R. and Rogers,M.B.
                                                                                                              gtttggggtaatcactcactggctctcagccttctaacactgcagccccttaatacagtt 1748
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AUTHORS
TITLE
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DLKKQCDVLVFEFEEVIEDWTRNHQEEDLTFETCANHVLKGKOTSCLAEQWSGKKGDT
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                                                                                                                                                          Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 2 Row: m Column: 12 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6002306. Location/Qualifiers
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cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortiu DNA Sequencing by: Institute for Systems Biology http://www.systemsbiology.org contact: amadandsystemsbiology.org Anup Madan, Rachel Dickhoff, Jessica Fahey, Steph Greene, Mark Ketteman and Anuradha Madan
                                                                                                                                                                                                                                                                             1. .1422
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/tissue_type="Colon, adenocarcinoma"
/clone_lib="NIH_MGC_15"
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Pred. No. 4.8e-164;
0; Mismatches 139;
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78. .914
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Submitted (29 MAY-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                             gtttggggtaatcactcactggctctcagccttctaacactgcagccccttaatacagtt 1748
                                         cogtgtccacccactcctcctgaggacgcctcatgctctgcccagcccttctcccagggc 1508
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    GGAGGAGCAGAGGCAGCTCTTTCTACACAGTCCCCCTCACGAGCTCCGGGGTCCACC 1181
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BC008898
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 1422)
Strausberg, R.
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Contact: MGC help desk
Email: cgapbs.r@mail.nih.gov
Tissue Procurement: ArC.
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Length 1422;

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DEFINITION

RESULT BC008898 LOCUS

ORGANISM

VERSION KEYWORDS SOURCE

AUTHORS TITLE JOURNAL

REMARK COMMENT

REFERENCE

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484 507 S

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AALGGKKSKKKSSRAKAAGGRSSSSKQRKELGGLEGDPSPEEDEGIOKASPLTHSPPD
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/tissue_type="Colon, adenocarcinoma"
/clone_lib="NIH_MGC_15"
/lab_host="DH10B-R"
                                                                                                                                                                                                                         Score 691.6; DB 9;
Pred. No. 4.8e-164;
0; Mismatches 139;
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                                    /note="Vector: pOTB7"
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/codon_start=1
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IMAGE:2959532, mRNA, complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contact: amadan@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Ketteman and Anuradha Madan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Euteleostomi;
Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (29-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                                AGCAGTGTGATGTGCTGGTGGAAGAGTTTGAGGAGGTGATCGAGGACTGGTACAGGAACC
                                                                                                                                            CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Institute for Systems Biology http://www.systemsblology.org
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Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC Project URL: http://mgc.nci.nih.gov
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/clone="MGC:4122 IMAGE:2959532"
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Mammalla, Eutheria, Primates,
1 (bases 1 to 1422)
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BC008961
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Direct Submission
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AUTHORS
TITLE
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/product="Unknown (protein for MGC:3530)"
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/db_xref="G1:3335208"
/translation="MDSMPEPASRCLLLLPLLLLLLLLLPAPELGPSQAGAEENDWVR
                                                                                                                                                                                                                                                                                                                                      bp mRNA linear PRI 12-JUL-2001
IMAGE:2819660, mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 9 Row: o Column: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LPSKCEVCKYVAVELKSAPEETGKTKEVIGTGYGILDQKASGVKYTKSDLRLIEVTET
ICKRLLDYSLHKERTGSNRFAKGMSETFETLHNLVHKGVKVVMDIPYELMNETSAEVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EC Cancer Agency, Vancouver, BC, Canada info@bogsc.bc.ca Steven Jones, Jennifer Asuno, Ian Bosdet, Yaron Butterfield, Steven Jones, Jennifer Asuno, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saedii, Jacqueline Schein, Duane Smallus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 5729791. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1720)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (12-MAR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                           748 AGAAGTCCAAGAAGAAGAGCAGCAGGCCAAGGCAGCAGCGGCAGGAGTAGCAGCAGCA
                                         agcagaaggaactggggggcctgggggaggatgccaacgccgaggaggaggaggtg
                                                                                                                 839 tgcagaaggcatcgccctcccacacagccccctgatgagctgtgagcccagcttagtg
                                                                                                                                     CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
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/clone_lib="NIH_MGC_7"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC Project URL: http://mgc.nci.nih.gov
Contect: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MGC:3530 IMAGE:2819660"
                                                                                                                                                                                                                     CTCTGTGAGGCCCTGATTTTGAAGCTGAGGA 963
                                                                                                                                                                                               teettgaateaagaeeeetgaetteagagettggga 934
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BC004423
BC004423.1 GI:13325207
MGC.
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DLKKQCDVLVEEFEEVIEDWYRNHQEEDLTEFLCANHVLKGKDTSCLAEQWSGKKGDT
AALGGKKSKKKSSRAKAAGGRSSSSKQRKELGGLEGDPSPEEDEGIQKASPLTHSPPD
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                                                                                              Length 1720;
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                                                                                            37.6%; Score 691.6; DB 9;
llarity 84.5%; Pred. No. 4.8e-164;
Conservative 0; Mismatches 139;
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     TTGAGGAAACCGCCAAGACCAAGGAGGTGATTGGCACGGGCTATGGCATCCTGGACCAGA
                            ccaagggtatgtcggagacctttgagacgctgcacaacctagtccacaaaggggtcaagg
                                                                                                                                                                           tggtgatggatatcccctatgagctgtggaacgagacctcagcagaggtggctgacctca
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Algate, P.A.
Ovarian tumor-associated sequences
Patent: WO 0151513-A 1320 19-JUL-2001;
CORIXA CORPORATION (US)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
136 c 172 g 106
                                                                                                                                                                                                                                                                         Location/Qualifiers
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Best Local Si
Matches 441)
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LPSKCEVCKVVAVERSAFEETGKTKEVIGTGYGILDQKASGVKYTKSDLRLTEVTET
ICKRLLIIACTRRGPAAIDLPRACQRPLRHYTTWYTKGSRW
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                                                              PRI 18-DEC-1997
                                                                                                                                                                                    Kidwai, A.S.,
and Ross, C.A.
brain
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Margolls, R.L., Abraham, M.R., Gatchell, S.B., Li,S.H., Kidwai, A.S.,
Bragolls, R.L., Abraham, M.R., Gatchell, S.B., Li,S.H., Kidwai, A.S.,
Breschel, T.S., Stine, O.C., Callahan, C., McInnis, M.G. and Ross, C.A.
Direct Submission
Submitted (02-DEC-1996) Psychiatry, Johns Hopkins Univ. Sch. of
Med., 600 N. Wolfe Street, Meyer 2-181, Baltimore, MD 21205, USA
Location/Qualifiers
                                                                                                                                                  Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
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Margolis, R. L., Abraham, M.R., Gatchell, S.B., Li, S. H., I Breschel, T.S., Stine, O.C., Callahan, C., McInnis, M.G. & CDAS With long CAG trinucleotide repeats from human 14 Hum. Genet. 100 (1), 114-122 (1997)
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Pred. No. 2.5e-113;
0; Mismatches 79;
1238 CCTCTGTCCTGAGCCCCTGATTTTGAAGCTGAGGA 1273
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                                                             962 bp mRN complete cds.
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                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="polyleucine rich" /codon_start=1
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/rpt_type=tandem
                                                                      Homo sapiens CTG4a mRNA,
U80744
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388. .819
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252 c
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/gene="CTG4a"
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il Similarity 87.3%;
549; Conservative
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Mammalia; Eutheria; P
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ilarity 84.0%;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bummalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dasses 1 to 580)

Algate, P. A. and Mannion, J.
                                                                                                                                                                                                                                                                                                                                                                             Compositions and methods for the therapy and diagnosis of ovarian
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241 GGTCAAGGTGGTGATGGACATCCCCTATGAGCTGTGGAACGAGACTTCTGCAGAGGTGGC 300
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                    474 ggtcaaggtggtgatggatatcccctatgagctgtggaacgagacctcagcagaggtggc
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Pred. No. 2.4e-93;
0; Mismatches 49;
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                                                                                                                                                                                                                                           Sequence 1232 from Patent WO0157207. AX209392.1 GI:15423815
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Location/Qualifiers
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al Similarity 90.0%;
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/translation="Heevvmdipyelwnetsaevadlkkocdvlveepeeviedwyrn
Hoeedlteficanhvlkgkdfsclaegwsgkkgdtaalggkkskkkssrakaaggrss
Sskorkelgglegdpspeedegiokasplthsppdel"
263 c 268 g 154 t
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (22-JAN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 11 Row: h Column: 23
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contact: amadan@systemsblology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anurac
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
gggaaaggacacgagttgcctagcagagcggtggtctggcaagaagggggacatagcctc
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Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
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/protein.id="AAH22093.1"
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Contact: MGC help desk
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Pred. No. 7.6e-73;
0; Mismatches 68
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Homo sapiens, clone IMAGE:3534003,
BC022003
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/lab_host="DH10B-R"
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/db_xref="taxon:9606"
/clone="IMAGE:3534003"
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Primates; C
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15.4%;
86.7%;
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Matches 338; Conserv
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/protein_id="AAF28907.1"
/protein_id="AAF28907.1"
/db_xref="G1:684108"
/translaten="NETSAEVADLKKQCDVLVEEFEEVIEDWYRNHQEEDLTEFLCAN
HVLKGKDTSCLAEOPASCKGDTAALGGKKSKKKSSRAKAGGRSSSSKQRKELGGLRE
TPAPRRMRASRRHPLSHTAPLMSSEPTQHPVLRPSSLKSE"
151 c 169 9 91 t
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Submitted (14-MAY-1999) Shanghai Institute of Hematology, Shanghai Second Medical University, Rui-Jin Hospital, 197 Rui-Jin Road II, Shanghai 200025, P. R. China
Location/Qualifiers
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Zhang, V. Hominidae; Homo.
Zhang, V.H., Ye, M., Zhou, J., Shen, Y., Wu, X.Y., Guan, Z.O., Wang Fan, H.Y., Mao, Y.F., Dai, M., Huang, Q.H., Chen, S.J. and Chen, Z. Unpublished
                                                                                                                                                                                                                                                                                                        aggacacgagttgcctagcagagcggtggtctggcaagaagggggacatagcctcctgg
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/tissue_type="cord blood"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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AC074220 89855 bp DNA linear HTG 25-JAN-2002 Mus musculus chromosome 17 clone RP23-76I16 strain C57BL6/J, WORKING DRAFT SEQUENCE, 38 unordered pieces.
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Han, J., Montgomery, K.T., Grills, G., Lee, E., Long, J., Pomerantz, R., Ioshikhes, I.P., Shim, C., Decker, J., Thomas, E., Perera, A., High Throughput Mouse Sequencing
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Han, J., Montgomery, K.T., Grills, G., Lee, E., Long, J., Pomerantz, R., Icshikhes, I.P., Shim, C., Decker, J., Thomas, E., Perera, A., Gordon, M., Goltz, J.S. and Kucherlapati, R. Direct Submission
Submitted (20-JUL-2000) Department of Molecular Genetics, Albert Bintean College of Medicine Genome Center, 1300 Morris Park Ave., On Apr 28, 2001 this sequence version replaced 91:11276104.
                                                                                                                                                                                                                                                                                                                                              802
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    Length 612;
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Sequencing vector: pUCl9; L08752
Chemistry: Dye-terminator B1g Dye; 100%
Score 284; DB 9;
Pred. No. 6.6e-61;
0; Mismatches 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Harvard Partners Genome Center
Center Code: HPGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: gnktm@capecod.bwh.harvard.edu
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HTG; HTGS_PHASE1; HTGS_DRAFT.
house mouse.
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g of 907 bp in length
f unknown length
of 1633 bp in length
when we length
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bp in length
                       in length
                                                                                                                                                                                                             unknown length
of 1417 bp in length
                                                                                        of 1817 bp in length
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88976: contig of 749 bp in length
88996; gap of unknown length
89855: contig of 859 bp in length.
                                                                        Length
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// note="assembly_name:Contig145"

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// note="assembly_name:Contig144"

// 13945. .18990
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/note="assembly_name:Contig135"
44151. .47059
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60642. .62255
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/note="assembly_name:Contig130"
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/note="assembly_name:Contig124"
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/note="assembly_name:Contig123"
69199. .70095
                     of 1311 bp in the contract of 2076 bp in
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49517. .52236
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52257. .54270
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/note="assembly_name:Contig126"
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/chromosome="17"
/clone="RP23-76116"
/sex="male"
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/organism="Mus musculus"
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                                                                                      Quality coverage: agarose-FP - N/A Quality coverage: 5.1 x in Q20 bases; sum-of-contigs estimation
                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 38 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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contig of 5942 bp in length
gap of unknown length
contig of 5046 bp in length
gap of unknown length
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y of 1706 bp in length
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bp in length
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of 810 bp in length
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of 2335 bp in length
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of 1529 bp in length
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*Consensus quality: 79355 at least Q20
*Consensus quality: 75365 at least Q30
*Consensus quality: 69022 at least Q40
Estimated insert size: agarose-FP - N/A
**Estimated insert size: 89115 - sum-of-contigs
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 746) Ota, T., Isogai, T., Nishikawa, T., Kawai, Y., Sugiyama, T. and Hayashi, K.
                                                                                                                                                                                                   gaggactggcagcaaccggtttgccaagggtatgtcggagacctttgagacgctgcacaa 458
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                                                 gttaattgaagtcactgagaccatttgcaagaggcttctggactacagcctgcacaagga
 ctatggcatcctggacgggaagggctctggagtcaag---tacaccaagtcggacttacg
                     195 GCAGGTGCTGGATACAGGCAAGAGAAGAGACACGTGCCTTACAGCGTTTCAGAGACAAG
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Patent: EP 1067182-8 538 10-JAN-2001;
Helix Research Institute (JP)
Location/Qualiflers
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/db_xref="taxon:9606"
142 c 251 g 149
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/note="assembly_name:Contig121"
71842. 73506
/note="assembly_name:Contig120"
73527. 74749
/note="assembly_name:Contig119"
74770. 75963
/note="assembly_name:Contig119"
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Pred. No. 1.4e-29;
0; Mismatches 228;
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7016="assembly_name:Contigl17"
77926. 79236
79257. 30132
79257. 30132
7040="assembly_name:Contigl16"
79257. 30132
7040="assembly_name:Contigl15"
81353. 81369
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'note-"assembly_name:Contig122"
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Khodadoust, M.M.
MSP-5 nucleic acid molecules and us.
Patent: US 6204013-A 3 20-MAR-2001;
Location/Qualiflers
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AR142811.1 GI:15104097
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Best Local Similarity 99.5%;
Matches 197; Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                       gttaattgaagtcactgagaccatttgcaagaggcttctggactacagcctgcacaagga
                                                                                                                                          372 GCGCAAGGGCTCACTGAGATATGCCAAGGGTCAGAGTCAGACCATGGCAACACTGAAAGG
                                                                                                                                                                                      cctagtccacaaaggggtcaaggtggtgatgtggatatcccctatgagctgtggaacgagac
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Novel polypeptide
Patent: JP 2001029090-A 4 06-FEB-2001;
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/db_xref="taxon:9606"
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OS HOMO Sapiens (human)
PN JP 200102990-A/4
PD 06-FEB-2001
PF 19-MAY-2000 JP 2000147530
PR YASUAKI ITO, SHINICHI MOGI, HI
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Submitted (19-DEC-2001) Cancer Genomics Office, National Cancer
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                           3;
Length 747;
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Homo sapiens, clone IMAGE:4991480, mRNA, partial cds.
BC019903
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                   Pred. No. 1.4e-29;
0; Mismatches 228;
    9
  DB
  Score 160.2;
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Tissue Procurement: ATCC
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Query Match 8.7%;
Best Local Similarity 57.3%;
Matches 310; Conservative
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DGEBKTEGEEEGEEEEEEEEEGKMYKTGSHPKLDREDL"
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Sequencing Center Contact code: BCW HGSC Contact code: BCW HGSC Contact: amg@bcm.tmc.edu/cdna/Contact: amg@bcm.tmc.edu Gunarathe, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M., Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M. Richards, S., Gibbs, R.A.
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/protein_id="AAH19903.1"
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/clone="IMAGE:4991480"
/tissue_type="Placenta, choriocarcinoma"
/clone_lib="NHH MGC_10"
/lab_host="Dh108"
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Matches 310; Conservative
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Copyright (c) 1993 - 2000 Compugen Ltd.
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ALIGNMENTS

|          | BH332134 558 bp DNA linear GS 03-DEC-2001 | CH230-201K14.TJ CHORI-230 Segment 1 Rattus norvegicu |           |         | GSS.     | Norway rat. | Rattus norvegicus | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1; | a; Eutheria; Rodentia; | Rattus. |           |         | A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riaas, F., de | Jong, P. and Fraser, C.M. |       | Unpublished | Other_GSSs: CH230-201K14.TV | Contact: Shaying Zhao | Department of Eukaryotic Genomics | The Institute for Genomic Research | 9712 Medical Center Dr., Rockville, MD 20850. USA | Tel: 301 838 0200 | Fax: 301 838 0208 | Email: szhao@tigr.org | Clones are derived from the rat BAC library CHORI-230 | (http://www.chor1.org/bacpac/rat230.htm). For BAC 11brary | availability, please contact Pieter de Jong (pdejong@mail.cho.org). | Clones may be purchased from BACPAC Resources | (http://www.chori.org/bacpac/or ering_information.htm). BAC end | page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html | Plate: 201 row: K column: 14 | Seq primer: SP6 | Class: BAC ends. |          |        | /organism="Rattus norvegicus" | /strain="bn/ssnhad/mcw" |
|----------|---|--|-----------|---------|----------|-------------|-------------------|---|------------------------|---------|-----------|---------|---|---------------------------|-------|-------------|-----------------------------|-----------------------|-----------------------------------|------------------------------------|---|-------------------|-------------------|-----------------------|---|---|---|---|---|---|------------------------------|-----------------|------------------|----------|--------|-------------------------------|-------------------------|
| BH332134 | LOCUS                                     | DEFINITION   | ACCESSION | VERSION | KEYWORDS | SOURCE      | ORGANISM          |   |                        |         | REFERENCE | AUTHORS |   |                           | TITLE | JOURNAL     | COMMENT                     |                       |                                   |                                    |   |                   |                   |                       |   |   |   |   |   |   |                              |                 |                  | FEATURES | sonrce |                               |                         |
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BH332134 CH239-201
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BE393833 601312107
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BE95105 601208484
BE908458 601503090
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BH332134
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BGG27656

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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs remail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LIML) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                            9
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CHORI-230 Rat (BN/SSNHSd/MCW) BAC library produced by pieter de Jong"
1 166 c 166 g 97 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                    174
                                                                                                                                                                                                                                                                                                                                                                                              241
                                                                                                                                                                                                                                                                                                                                                                                                                         175 gctctctgattgggtgagatgggaaaaaaaaaaaaaqatagttctctctcattggctataaagc 234
                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                         1 acagaaaacaagaaacaaaaaccatgaaagatagtctgttatccagggc-tagaatgccc 59
                                                                                                                                                                                                                                                                                                                                                                 119 act----gagcctcctttagctggcagtgatatcgctatagggcgccaaagccaccatcc
                                                                                                                                                                                                                                                                                                                                                                                182 TCTCCCAGAACCTCCGTTAGATGGCCGTGAGATCGCTATAGGGCGCCAAATCCACCATCC
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                                                                                                                                                                             Score 295.2; DB 12; Length 558; Pred. No. 5.5e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54; Indels
                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
Other_ESTs: 2819660.3prime
Contact: Robert Strausberg, Ph.D.
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AW245217
AW245217.1 GI:6588210
                                                                                                                                                                                  62.7%;
85.7%;
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/cloue="nrawce:colsoou"
/clone_lib="NIH_MGC_7"
/tissue_type="small cell carcinoma"
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CooRI; cDNA made by oligo-dT priming, Directionally
cloned into EcoRI/XhoI sites using the following 5,
cloned into EcoRI/XhoI sites using the following 5,
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert Size 1:8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (Gniversity of
California, Berkeley) using zap-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
58 a 125 c 146 g 77 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washingtion Genome Center. Vector Trimming: cross_match from University of Washingtion Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washingtion Genome Center. http://www.genome.washington.edu http://www.genome.washington.edu Plate: LLCM2 row: C column: 21 High quality sequence stop: 361.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ggcagtgatatcgctatagggcgccaaagccaccatccgctctctgattgggtgagatgg 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               202 CIGCGCCGTCCGCGGGCCTTGGTCGCTTTGAAGGCGGGCCTGCGACGAGGAGGGC 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   376
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       257 ttgngtcgccgcggggccttggtcggtttcgcaagccgctagaggctaccgggcgagggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               262 GGGCGGGGGGCTAGCTGTTGTCGTGGTTGCTCGGAGGTCCCGGAAGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      317 egggeeggagetegeegttgeegtggttacceagagaeacgtgegeagteeeggaagegg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 9; Length 416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 159.8; DB 9; Length
Pred. No. 2.8e-25;
0; Mismatches 88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
/clone="IMAGE:2819660"
                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.98;
71.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 33.9 Best Local Similarity 71.6 Matches 239; Conservative
                                                                                                                                                                                                                                                        1. .416
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/clone_lib="NIH_MGC_19"
/clone_lib="NIH_MGC_19"
/tlswe_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2: ECORI; cDNA made by oligo-dT priming. Directionally cloned into ECORI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscribt II RT (Life Technologies).
Note: this is a NH_MGC Library."
                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammallan Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement. ATC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomicas, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM314 row: b column: 22
High quality sequence stop: 670.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ggcagtgatatcgctataggggcgccaaagccaccatccgctctctgattgggtgaggtgg 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197 gaaaaaaaaaaaaagategtteetettggetataaageagaegeegagegaaceattgg 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             166 CTGCGCCGTCGGCGTTGGTCCGCTTTGAAGGCGGGCTGCGGCTGCGAGGAGGAGGGC 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cgggccggagctcgccgttgccgtggttacccagagacacgtgcgcagtcccggaagcgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88;
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llarity 71.6%; Pred. No. 2.8e-25;
Conservative 0; Mismatches 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .676
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Best Local Simi
Matches 239;
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                          AUTHORS
TITLE
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                            1. .515
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/tasue_type="endometrium, adenocarcinoma cell line"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 676)
                                                                             Tissue Procurement, ATCC CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov. n column: 01 Plate: LLCM348 row: n column: 01 High quality sequence stop: 513.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137 ggcagigatatogctatagggogccaaagccaccatccgctctctgattgggtgaggg 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               317 cgggccggagctcgccgttgccgtggttacccagagacacgtgcgcagtcccggaagcgg 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         226 GGGCGGGGGGCTGTTGTCGTGGTTGCTCGGAGGCACGTGTGCAGTCCCGGAAGCGG 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ccgggggaagctcccgcgcgcgcgctgccggaaggaagcgccgccgggtccgctct 436
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Pred. No. 2.8e-25;
0; Mismatches 88
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Unpublished (1999)
Contact: Robert Strausberg, P
Email: cgapbs-rémail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
33.9%;
Best Local Similarity 71.6%;
Matches 239; Conservative
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AUTHORS TITLE JOURNAL REFERENCE

COMMENT

FEATURES

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Inquipulished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Toshiyuki and Plear Carninci (RIKEN)
Toshiyuki and Plear Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consorthum (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consorthum/LLNL at: http://image.llnl.gov
Plate: LLAM10726 row: h column: 22
High quality sequence stop: 716.
High quality sequence stop: 716.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /_ord="Organ: Drain; Vector: pBluescriptR (modified pBluescript K8+); Site_1: BamHI; Site_2: Salr-xhoI (gtcgag pBluescript K8+); Site_1: BamHI; Site_2: Salr-xhoI (gtcgag size-selected for average insert size 2:5 kb and normalized to R0T 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Garninci, in preparation). Library constructed by M. Brownstein (NHM/NHGRI, National constructed by Health). Note: this is a NIH_MGC Library."
         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       333
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                                                                   1 (bases 1 to 828)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 2.9e-25;
0; Mismatches 88; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="hippocampus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aggiccagcigagccaigagiccaigtcigagc
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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_95"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ф
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71.6%;
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Matches 239; Conservative
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BE908458
LOCUS
                    ORGANISM
                                                                                                        AUTHORS
TITLE
JOURNAL
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: pooled pancreas and spleen; Vector:
pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dr primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1:5 kb, insert size range 1-2.5 kb. Library is
confailzed and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025: Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;;
                                                                                                      Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
    Tissue Procurement: Life Technologies, Inc.
    CDNA Library Preparation: Life Technologies, Inc.
    CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
    DNA Sequencing by: Incyte Genomics, Inc.
    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
    http://image.lln.gov
    Plate: LLAM1570 row: 1 column: 18
    High quality sequence stop: 687.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             257 ttgngtcgcccgcgggccttggtcggttcgcaagccgctagaggctaccgggcgagggg 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  191 CTGCGCCGTCCGCGGCCTTGGTCGCTTTGAAGGCGGGCTGCGGCTGCGAGGAGGGGC 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 TAAAAAGATAG-----TCCTCCCATTAGCTAGAGAGCAAACCC-AGAAAGCTATTGG 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                    1 (bases 1 to 690)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cgggccggagctcgccgttgccgtggttacccagagacacgtgcgcagtcccggaagcgg
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    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 159.8; DB 10; Length 690;
Pred. No. 2.8e-25;
0; Mismatches 88; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gggtccggctgggccatggagtccatgtctgagc 470
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                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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/clone_lib="NIH_MGC_120"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab\_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA sequence.
BG704841
BG704841.1 GI:13978583
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al Similarity 71.6%;
239; Conservative
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Query Match Best Local S: Matches 239,

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RESULT BG704841

377

317

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437 371 DEFINITION

ACCESSION

VERSION KEYWORDS

BASE COUNT ORIGIN

2;

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Contact: nisc_mac@nhgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       can be found
                                                                                                              Craniata, Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov series: IRAL Plate: 27 Row: f Column: 20
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein
This clone has the following problem: incomplete processing.
Location/Qualifiers
                                                                                                                                                                          Strausberg, R. Direct Submission Direct Submission Submits of Health, Mammalian Submitted 30-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 GGAAAGGACTTTGCCATAGGTCGCTGAGGCCACCATCTGCTCTTACTGGCCAAGGGCG 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137 ggcagtgatatcgctatagggcgccaaagccaccatccgctctctgattgggtgagatgg 196
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                                                                                                                                                                                                                                                                                                                                                                                        CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 194 CTGCGCCGTCCGCGGGCCTTGGTCCGCTTTGAAGGCGGGCTGCGGCTGCGAGGGGGC
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Pred. No. 2.9e-25;
0; Mismatches 88; Indels 7;
                                                                                                                                                                                                                                                                                                            NIH-MGC Project URL: http://mgc.nc1.nlh.gov
Contect: MGC help desk
Emall: cgapbs-femall.nlh.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.nisc.nih.gov/
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491 g :
                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 1602)
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                       GI:15079962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.9%;
illarity 71.6%;
Conservative
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                                                                                          Homo sapiens
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  BC011767
BC011767.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site:
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Best Local S1
Matches 239;
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ORIGIN
                                                                                       ORGANISM
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TITLE
JOURNAL
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  ACCESSION
                    VERSION
KEYWORDS
SOURCE
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COMMENT
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                                                                                                                                          Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 848)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Onpublished (1999)

L Ontact: Robert Strausberg, Ph.D.

Emall: cgapps-remant: ATCC

CONTACT: Robert Strausberg, Ph.D.

Emall: cgapps-remant: ATCC

CONA Library Preparation: Life Technologies, Inc.

CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Plate: LLAM9711 row: c column: 23

High quality sequence stop: 697.

Location/Qualifiers

I Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Organism="Homo sapiens"
/db_xref="taxon:9606"
/clone=lib="NHL MAGE:3904846"
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/tissue_type="epithelioid carcinoma"
/lab_host="bulb8 (phage=resistant)
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Powerage insert size 1:1 kb. Library constructed by Life
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  601503090F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3904846 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137 ggcagtgatatcgctatagggcgccaaagccaccatccgctctctgattgggtgagatgg 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gaaaaaaaaaaagatagttcctctcattggctataaagcagacgccgagcgaacccattgg 256
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71.6%; Pred. No. 2.9e-25;
iive 0; Mismatches 88;
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1 237 c 276 g
                                                                BE908458.1 GI:10403057
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Matches 239; Conservative
                         sednence.
                                                                                                                                   Homo sapiens
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Matches 238
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                                                                                                                                                                                                            BI760437 1002 695 bp mRNA linear EST 25-SEP-2001 603045452F1 NIH_MGC_116 Homo sapiens CDNA clone IMAGE:5185596 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5;
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                                                                                                                                                                                                                                                                                                                                                                Eukaryotania Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I bases 1 to 695)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.W.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.W.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM11463 row: h column: 13
377 ccgggggaagctgctccgcgcgcgctgccggaagaagcgccgccggggtccgctctgctct 436
                                        314 CGAGGGGAAACTGCTCCGCGCGCGCGCGGGGGGGAGGAACCGCCCGGTCCTTTAGGGTCC 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194 tgggaaaaaaaaaaaagatagttcctctcattggctataaagcagacgagggaacccat 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 getggcagtgatategetatagggegeceaaagecaceateegetectgattgggtgaga 193
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Pred. No. 3.1e-25;
); Mismatches 90; Indels
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                                                                            0; Mismatches
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/clone_lib="NIH_MGC_l16"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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High quality sequence stop: 695.
Location/Qualifiers
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BI760437
BI760437.1 GI:15752015
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71.2%;
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Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s.wiemann@dkf2- heidelberg.de;
sequenced by LMU (Ludwig Maximilians University,
Munich/Germany) within the cDNA sequencing consortium of the German
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AL134371 615 bp mRNA linear EST 25-FEB-2000 DKFZp547B155_r1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547B155 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 615)
Blum, H., Bauersachs, S., Mewes, W., Weil, B. and Wiemann, S.
EST (Blum, H., Bauersachs, S., Mewes, H.W., Weil, B. and Wiemann, S.)
Unpublished (1999)
Contact: Blum H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     No s1 sequence available.
This clone (DKFZp547B155) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de.
Location/Qualifiers
153 TGGCTGCGCCGTCCGCGGGCCTTGGTCCGCTTTGAAGGCGGGCTGCGGCTGCGAGAGGAG 212
                                                                                                                                                                                       ttgngtcgcccgcggggccttggtcggtttcgcaagccgctagaggctaccggggcgagggg 316
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                                               gaaaaaaaaaaagatagttcctctcattggctataaagcagacgccgagcgaacccattgg
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/db_xref="taxon:9606"
/clone="DKF2p547B155"
/clone_lib="547 (synonym: hfbr1)"
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llarity 71.3%; Pred. No. 6.3e-25;
Conservative 0; Mismatches 89;
                                                                                                                                                                                                                                                                   434 tctgggtccggctgggccatggagtccatgtctgagc 470
                                                                                                                                                                                                                                                                                               333 TCCGGGCCCGGCCGGGCCATGGATTCAATGCCTGAGC 369
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/lab_host="X1-2blue"
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AL134371.1 GI:6602558
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/clone_libractions
/tissue_type="leukocyte"
/tissue_type="leukocyte"
/tissue_type="leukocyte"
/tab_nost="bh108"
/note="vector: pcWv-SPORT6; Site_1: NotI; Site_2: EcoRv
/note="vector: pcWv-SPORT6; Site_1: NotI; Site_2: EcoRv
(destroyed); RNA Source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EcoRv site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 027. Note:
this is a NIH,MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CLONG distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mmge.llnl.gov
Plate: LLAM11537 row: e column: 11
High qualify Sequence stop: 690.
I. 695
                                                                                                                                                                                                                                                                                                                                                                                                                            B1906932 695 bp mRNA linear EST 16-OCT-200
603064743F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5213938 5',
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Mammalia; Eutheria; Primațes; Catarrhini; Hominidae; Homo.
1 (bases 1 to 695)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         256
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                                   377 ccgggggaagctgctccgcgcgcgcgctgccggaggaagcgccgccgggtccgctctgctct 436
                                                                                                                                                   10 CGAGGGAAACTGCTCCGCGCGCGCGCGGGAGGAGCGCCCCGGTCCTTTAGGGTCC 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 695)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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317 cgggccggagctcgccgttgccgtggttacccagagacacgtgcgcagtcccggaagcgg
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                                                                                                                                                                                                                            370 GGGCCCGGCCGGCCATGGATTCAATGCCTGAGC 403
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/db_xref="taxon:9606"
/clone="IMAGE:5213938"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
BI906932
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/clone_lib="NHH_MGC_122"
/lab_host="DHIOB"
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
Site_l: NotI; Site_2: ECORV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen; and 20-22 week male spleens. Library is oligo-dr
primed and directionally cloned (ECORV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7
                                                                                                                                                                                                                                                                                                                                                                                                  BI766238 11near EST 25-SEP-2001 603052885F1 NIH_MGC_122 Homo saplens cDNA clone IMAGE:5202525 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Theyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
                                                                                                                                                                1 (bases 1 to 706)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
257 ttgngtcgcccgcgggccttggtcggtttcgcaagccgctagaggctaccggggcgagggg 316
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                   153 CTGCGCCGTCCGCGCTTGGTTTGAAGGCGGGCTGCGGCTGCGGAGGGGC
                                                                                                         cgggccggagctcgccgttgccgtggttacccagagacacgtgcgcagtcccggaagcgg
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Pred. No. 6.4e-25;
....matches 89; Indels
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203 c 233 g 139 t
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                                                                                                                                                                                                                                                                         333 GGCCCGGCCGGCCATGGATTCAATGCCTGAGC 366
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/db_xref="taxon:9606"
/clone="IMAGE:5202525"
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Matches 238; Conservative
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602748652F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4901437 5',
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I (bases 1 to 827)

II (bases 1 to 827)

NHF-MGC http://mgc.nci.nlb.gov/.

National institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: ATCC
                                                                                                                    cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Theyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://mgc.llnl.gov column: 14
                                             136 TAAAAAGATAG-----TCTTCCCATTAGCTAGAGAGCAAAC-CCCAGAAAGCCTATTGG 188
                                                                                                                                                                                                                                              309 CGAGGGGAAACTGCTCCGCGCGCGCGCGGAGGAACCGCCCGGTCCTTTAGGGTCC 368
                                                                                                                                                                                                                                                                                                                                                                            377 ccgggggaagctgctccgcgcgcgctgccggaggaagcgccgccggggtccgctctgctct 436
gaaaaaaaaaaagatagttcctctcattggctataaagcagacgccgagcgaacccattgg
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High quality sequence stop: 535.
Location/Qualifiers
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/db_xref="taxon:9606"
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Gaps

Indels

238; Conservative

Matches

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Anote—Torgan: B-cells; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; CDNA made by oligo-dT priming.

Site_2: EcoRI; CDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH_MOC Library."
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Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 951)
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NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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137 ggcagtgatatcgctatagggcgccaaagccaccatccgctctctgattgggtgagatgg 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300 CGAGGGGAAACTGCTCCGAGCGCGCGCGGGAGGAACCGCCCGGTCCTTTAGGGTCC 359
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Clone distribution: MGC clone distribution information can lfound through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lll.gov
Plate: LLCM1695 row: k column: 23
High quality sequence stop: 831.

1. 951
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                                                                                                                                                             127 TAAAAAGCTAG-----TCCTCCCATTAGCTAGAGAGCAAACCCC-AGAAAGCCTATTGG
                                                                                                                                                                                                                                                   gaaaaaaaaaaagatagttcctctcattggctataaagcagacgccgagcgaacccattgg
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/clone_lib="NIH_MGC_48"
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BG755172
BG755172.1 GI:14065825
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Best Local Similarity
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/clone="IMAGE:5239791"
/clone="IMAGE:5239791"
/clone="IMAGE:5239791"
/clone="Organ: Drain; Vector: pCMV-SPORT6; Site_1: NotI;
/lab_host="DH10B"
/lab_host="DH1B"

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BI523540 E1523540.1 GI:15348332
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMil604 row: j column: 16
High quality sequence start: 3
High quality sequence stop: 724.
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NIH-WGC http://mgc.ncl.nih.gov/.
                                                                                                                         317 cgggccggagctcgccgttgccgtggttacccagagacacgtgcgcagtcccggaagcgg 376
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                                                                                                                                                                                                                                                                                             142 TAAAAAGATAG-----TCTTCCCATTAGCTAGAGAGCAAC-CCCAGAAAGCCTATTGG 194
                                                                                                                                                                                                                                                                                                                                                                                                                          195 CTGCGCGGTCCGGGGCCTTGGTCGCTTTGAAGGCGGGCTGCGGCTGCGAGGGGGC 254
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                                                                      Gaps
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      DB 10; Length 951;
                                                                   Indels
Score 158.2; DB 10;
Pred. No. 6.4e-25;
0; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 437 gggtccggctgggccatggagtccatgtctgagc 470 | 11 | 11 | 11 | 11 | 11 | 11 | 1375 GGGCCGGGCCGTGGATTCAATGCCTGAGC 408
   33.68;
71.38;
                              Best Local Similarity 71.3
Matches 238; Conservative
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BI523540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
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AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                        197
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                                                                                                     Gaps
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                                                                                                     84; Indels
                                                                         DB 10;
                                                                      Query Match 33.2%; Score 156.2; DB 1
Best Local Similarity 71.9%; Pred. No. 1.8e-24;
Matches 233; Conservative 0; Mismatches 84
NIH_MGC Library.
241 g 146
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May 24, 2002, 00:20:16; Search time 121.39 Seconds (without alignments) 953.072 Million cell updates/sec
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Sequence 1, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 2, Appli
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                                                                                                          US-09-696-686-50
471
1 acagaaaacaagaaacaaaa.....atggagtccatgtctgagct 471
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Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-306-691B-14
US-09-209-668-10
US-09-356-952-8
US-09-773-816-1
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US-08-460-907B-1
US-08-463-179A-1
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                                                                                                                                                                                        383533 seqs, 122816752 residues
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Maximum Match 100%
Listing first 45 summaries
                                          OM nucleic • nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Sequence 3. Application US/08628829A

Fatent No. 6333170

GENERAL INFORMATION:
APPLICANT: Johnson, Gary L.
TITLE OF INVENTION: Method And Product For Regulating Cell Responsiveness To Exter
FILE REFERENCE: CPI-004DVCP3

CURRENT FILING DATE: 1996-04-05

EARLIER FILING DATE: 1996-04-05

EARLIER FILING DATE: 1996-04-05

EARLIER PILING DATE: 1994-10-14

EARLIER PILING DATE: 1994-10-14

EARLIER FILING DATE: 1995-04-24

EARLIER FILING DATE: 1995-04-24

EARLIER APPLICATION NUMBER: 08/410,602

EARLIER APPLICATION NUMBER: 08/410,602

EARLIER APPLICATION NUMBER: 08/410,602

EARLIER FILING DATE: 1995-04-24

EARLIER FILING DATE: 1995-04-24

EARLIER FILING DATE: 1995-04-24

EARLIER FILING DATE: 1995-06-06

NUMBER OF SEQ ID NOS: 25

SOFTWARE: PATEUR VET. 2.0
            Sequence 1, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 182, Appli
Sequence 18, Appli
Sequence 15, Appli
Sequence 8, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
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Pred. No. 0.067;
0; Mismatches 59; Indels 0
                    US-08-924-847A-1
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US-09-120-052-1
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US-08-06-452-6
US-08-08-481-970-8
US-08-897-719-8
US-08-103-840A-2
US-09-103-840A-2
US-08-813-940-3
US-09-103-840A-1
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 6244
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Matches 74; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: CDS
; LOCATION: (1)..(4779)
US-08-628-829-3
 6.90
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LENGTH: 5539
US-08-628-829-3
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CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 ccgcgagagaaaatggcggcggcggcggcgatcgcgcctcgtcgtcgggattcccgggc 62
                             GENERAL INFORMATION:
APPLICANT: CADUS PHARMACEUTICAL CORPORATION
TITLE OF INVENTION: HUMAN MEKK PROTEIN AND NUCLEIC ACID MOLECULES;
TITLE OF INVENTION: HUMAN MEKK PROTEIN AND NUCLEIC ACID MOLECULES;
TITLE OF INVENTION: AND USES THEREFOR
FILE REFERENCE: CPI-085CPPC
CURRENT APPLICATION NUMBER: US/09/423,890
CURRENT ELING DATE: 1098-03-06
PRIOR FILING DATE: 1998-03-16
PRIOR FILING DATE: 1998-03-16
PRIOR FILING DATE: 1998-03-16
PRIOR FILING DATE: 1998-03-04
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PALENTIN VOICE: 2.0
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Cole, Susan P.C.
APPLICANT: Deeley, Roger G.
TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEIN
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, SUITE 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patentin Release #1.0, Version #1.25
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/966,923; 08/029,340
APPLICATION NUMBER: 27-0CT-1992; 8-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US/08/141,893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08141893
Patent No. 5489519
GENERAL INFORMATION:
Sequence 7, Application US/09423890 Patent No. 6312934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DeConti, Giulio A. Jr.
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Best Local Similarity 56.2%;
Matches 72; Conservative
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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STATE: MASSACHUSETTS
COUNTRY: USA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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; LOCATION: (15)..(4493)
US-09-423-890-7
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                                                                                                                                                                                                                                                                                                                          SEQ ID NO 7
LENGTH: 5253
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US-08-141-893-1
                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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309 gcgagggggggggggggggccgtcgccgttgccgtggttacccagagacacgtgcgcagtccc 368
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Patent No. 5766880
GENERAL INFORMATION:
APPLICANT: Cole, Susan P.C.
APPLICANT: Deeley, Roger G.
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                        Score 36.8; DB 1; Length 5011;
Pred. No. 0.22;
0; Mismatches 62; Indels 0.
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ZIP: K7L 3N6

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
RPLICATION NUMBER: US/08/463,092B
FILING DATE: 05-JUN 1995
CLASSIFICATION: 435
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PQI-002
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APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
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APPLICATION NUMBER: 08/141,893
FILING DATE: 26-0CT-1993
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APPLICATION NUMBER: 07/966,923
             REFERENCE/DOCKET NUMBER:
POI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPRX: (617) 227-5140
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5011 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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N: 435
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Best Local Similarity 54.4°
Matches 74; Conservative
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CLASSIFICATION: 435
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CITY: Kingston
STATE: Ontario
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US-08-141-893-1
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CLASSIFICATION: 435
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Patent No. 5766880

GENERAL INFORMATION:
APPLICANT: Cole, Susan P.C.
APPLICANT: Deeley, Roger G.
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
STREET: Queen's University at Kingston
STATE: Onlean's University at Kingston
STATE: Onlean's University at Kingston
STATE: Onlean's University at Kingston
STATE: CONFUTER READABLE FORM:
MEDIUM TYPE: Eloppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
PFILING DATE: 05-JUN-1995
CLASSIFICATION: 435
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7.8%; Score 36.8; DB 1;
Best Local Similarity 54.4%; Pred. No. 0.22;
Matches 74; Conservative 0; Mismatches 62;
              APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
CLEASIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Steeg, Carol Miernicki
REGISTRATION NUMBER: 39,539
REFERENCE/DOCKET NUMBER: 01546
TELEFONMUNICATION INFORMATION:
TELEFONMUNICATION INFORMATION: (613) 545-6853
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5011 base pairs
TYPE: nucleic acid
STRANDEDDESS: double
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APPLICATION NUMBER: 07/966,923
FILING DATE: 27-0CT-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/029,340
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: 196..4788
                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
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US-08-463-092B-1
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174 céccécécécécecaccédarecécricesédrantiques 233
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Sequence 1, Application US/08462109A

Sequence 1, Application US/08462109A

Sequence 1, Application US/08462109A

Patent No. 5882875

SENERAL INFORMATION:

APPLICANT: Cole, Susan P.C.

APPLICANT: Cole, Susan P.C.

TITLE OF INVENTION: MULTIDRUG RESISTANT TUMOR CELLS

NUMBER OF SEQUENCES:

CORRESPONDENCES:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 State Street, suite 510
CLASSIFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/141,893
FILING DATE: 26-0CT-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stee9, Carol Miernicki
REGISTRATION NUMBER: 39,539
REFERENCE/DOCKET NUMBER: 01546
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 545-6853
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5011 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,109A
FILING DATE:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: CDS
; LOCATION: 196..4788
US-08-463-0928-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: CDNA
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309 gcgaggggggggggggggggtcgccgttgccgtggttacccagagacacgtgcgcagtccc 368
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Patent No. 5891724
GENERAL INFORMATION:
APPLICANT: Deley, Roger G.
APPLICANT: Cole, Susan P.C.
TITLE OF INVENTION: METHODS FOR CONFERRING MULTIDRUG
TITLE OF INVENTION: RESISTANCE ON A CELL
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 36.8; DE
Pred. No. 0.22;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII text
                                                                   APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
FILING DATE: 08/141,893
FILING DATE: 26-0CT-1993
APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
ATTORNEY AGENT INFORMATION:
NAME: DECORTI, GIULIO A. Jr.
07/966,923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 7.8%;
Best Local Similarity 54.4%;
Matches 74; Conservative
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                                     27-0CT-1992
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APPLICATION NUMBER: US/
FILING DATE: 05-JUN-199
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STATE: Ontario
COUNTY: CANADA
ZIP: K7L 3N6
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CDNA
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APPLICANT: Cole, Roger G.
TITLE OF INVENTION: METHORS FOR IDENTIFYING
TITLE OF INVENTION: MULTIDRUG RESISTANT TUMOR CELLS
NUMBER OF SEQUENCES: 6
CORRESPONDENCES: ADMITTED FOR SECUENCES: ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 36.8; DB 2;
Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                               APPLICATION NUMBER:

APPLICATION NUMBER:

BAPALICATION NUMBER:

BATORNEY/AGBNT INFORMATION:

REGISTRATION NUMBER:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECAM:

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,109A
FILING DATE:
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 5011 base pairs
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| ||||||||| |||
234 CCCGCTCTGGGACTGG 249
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Best Local Similarity 54.49
Matches 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             196..4788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: cDNA
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; LOCATION: 196.
US-08-462-109A-1
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| Sequence 1, Application US/08463179A
| Sequence 1, Application US/08463179A
| Patent No. 6001563
| GENERAL INFORMATION:
| APPLICANT: Cole, Susan P.C.
| APPLICANT: Cole, Susan P.C.
| APPLICANT: Deeley, Roger G.
| TITLE OF INVENTION: METHODS FOR IDENTIFYING CHEMOSENSITIZERS
| NUMBER OF SEQUENCES: 6
| CORRESPONDENCE ADDRESS: ADDRESSE: LAHIVE & COCKFIELD
| STREET: 60 State Street, suite 510
| CITY: Boston Street, suite 510
| STREET: Massachusetts
| COUNTRY: USA |
| SIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 7.8%; Score 36.8; DB 2; Length 5011; Best Local SImilarity 54.4%; Pred. No. 0.22; Matches 74; Conservative 0; Mismatches 62; Indels 0
              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,907B
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
                                                   FILING DATE: 0.5-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION 1424
PRIOR APPLICATION NUMBER: 07/966,923
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/029,340
FILING DATE: 8 MAR-1993
CLASSIFICATION 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/11,893
FILING DATE: 26-0CT-1993
CLASSIFICATION: 424
PRIOR APPLICATION A14
PRIOR APPLICATION: 424
APPLICATION NUMBER: 08/407,207
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Steeg, Carol Miernick!
REGESTRATION NUMBER: 39,539
REFERENCE/DOCKET NUMBER: 01551
TELECOMMUNICATION INFORMATION:
TELEPAN: (613) 545-6853
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 5011 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              429 tctgctctgggtccgg 444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: CDS
; LOCATION: 196..4788
US-08-460-907B-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Deceley, Roger G.
APPLICANT: Cole, Sugan P.C.
TITLE OF INVENTION: METHODS FOR CONFERRING MULTIDRUG
TITLE OF INVENTION: METHODS FOR CONFERRING MULTIDRUG
TITLE OF INVENTION: MESISTANCE ON A CELL
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: PARTEC RESEARCH & DEVELOPMENT INNOVATIONS
STREET: Queen'S University at Kingston
STATE: Oneario
COUNTRY: CANADA
ZIP: KINGSTON
MEDIUM TYPE: Floppy disk
COMPUTER FEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
  CLASSIFICATION: 424

PRIOR APPLICATION DATA.
APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
CLASSIFICATION NUMBER: 08/141,893
FILING DATE: 26-007-1993
CLASSIFICATION NUMBER: 08/141,893
FILING DATE: 26-007-1993
CLASSIFICATION: 424
PRIOR APPLICATION: 613
FILING DATE: 20-MAR-1995
CLASSIFICATION NUMBER: 39,539
REFERENCE/DOCKET NUMBER: 31,539
REFERENCE/DOCKET NUMBER: 0151
TELEPHONE: (613) 545-6853
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5011 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08460907B
Patent No. 5891724
GENERAL INFORMATION:
27-0CT-1992
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196..4788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION:
US-08-460-907B-1
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369 ggaagcggccgggggaagctgctccgcgcgcggaggaagcgccgcgggtccgc 428
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7.8%; Score 36.8; DB 3; Length 5011;
Best Local Similarity 54.4%; Pred. No. 0.22;
Matches 74; Conservative 0; Mismatches 62; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08461384B

Sequence 1, Application US/08461384B

Patent No. 6025473

GENERAL INFORMATION:
APPLICANT: Cole, Susan P.C.
APPLICANT: Deeley, Roger G.
TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
STREET: Queen's University at Kingston
CITY: Kingston
STATE: Ontario
COUTTY: CANADA
ZIP: K71 3NG
COMPUTER READABLE FORM:
MULTIDRUG RESISTANCE PROMESTICE
COMPUTE: FILOSOPHICALIONS
COMPUTE: 
COMPUTER: IBM PC compatible
OPERATING SISTEM: PC-DOS/MS-DOS
SOGFWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,179A
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/966,923
FILING DATE: 27-07-1992
APPLICATION NUMBER: 08/029,340
FILING DATE: 28-MAR-1993
APPLICATION NUMBER: 08/11,893
FILING DATE: 20-07-1993
APPLICATION NUMBER: 08/41,893
FILING DATE: 20-07-1993
APPLICATION NUMBER: 08/40,207
FILING DATE: 20-07-1993
APPLICATION NUMBER: 08/40,207
FILING DATE: 20-07-1993
APPLICATION NUMBER: 9503
APPLICATION NUMBER: 995
ATORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 91.503
REFERENCE/DOCKET NUMBER: PQI-002CPB
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 5011 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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196..4788
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LOCATION:
US-08-463-179A-3
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US-08-461-384B-1
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Patent No. 6001563
GENERAL INFORMATION:
APPLICANT: Cole, Susan P.C.
APPLICANT: Cole, Susan P.C.
TITLE OF INVENTION: METHODS FOR IDENTIFYING CHEMOSENSITIZERS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.8%; Score 36.8; DB 3; Length 5011; Best Local Similarity 54.4%; Pred. No. 0.22; Matches 74; Conservative 0; Mismatches 62; Indels 0;
                                                                                                                                                                                                              CHERATION SISTING CONTROLL OF CONTROLL OF COURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/463,179A
FILING DATE:
FILING DATE:
APPLICATION DATA:
APPLICATION NUMBER: 08/029,340
FILING DATE: 27-0CT-1992
APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
APPLICATION NUMBER: 08/407,207
FILING DATE: 26-0CT-1993
APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
ATTONNEY/ACENT INFORMATION:
NAME: DECONTL, GILLIO A. JT.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: 901-002CP8
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy disk
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                                                              COMPUTER READABLE FORM:
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196..4788
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LOCATION:
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309 gcgaggggcgggccggagctcgccgttgccgtggttacccagagacacgtgcgcagtccc 368
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Patent No. 6053621

CENERAL INFORMATION:
APPLICANT: Deeley, Roger G.
APPLICANT: Cole, Susan P.C.
TITLE OF INVENTION: ANTIBODIES TO A MULTIDRUG RESISTANCE PROTEIN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 5011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: ADATED RESEARCH & DEVELOPMENT INNOVATIONS
STREET: Queen's University at Kingston
CITY: Kingston
STATE: Ontario
COUNTRY: CANADA
ZIP: K7L 3NG
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: ASCII text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
7.8%; Score 36.8; DB 3;
Best Local Similarity 54.4%; Pred. No. 0.22;
Matches 74; Conservative 0; Mismatches 62;
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CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/08/407,207A
FILING DATE: 20-MAR-1995
     FILING DATE: 05-JUN-95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/966,923
FILING DATE: 8-70CT-1992
APPLICATION NUMBER: 08/02,340
FILING DATE: 8-70CT-1993
APPLICATION NUMBER: 08/14,893
APPLICATION NUMBER: 08/407,207
APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Steeg, carch Miernick!
REGISTRATION NUMBER: 39,539
REFERENCE/DOCKET NUMBER: 39,539
REFERENCE/DOCKET NUMBER: 39,539
TELEPAX: (613) 545-6853
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5011 base pairs
TELEGTH: 5011 base pairs
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234 CCCGCTCTGGGACTGG 249
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CDNA
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US-08-461-384B-3
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Patent No. 6025473
GENERAL INFORMATION
GENERAL INFORMATION
FAPPLICANT: Cole, Susan P.C.
APPLICANT: Deeley, Roger G.
TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
STREET: Queen's University at Kingston
CITY: Kingston
STATE: Ontario
COUNTRY: Canada
COUNTRY: Canada
COUNTRY: Canada
COUNTRY: Canada
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PEDOPOS/MS-DOS
CORTABABE. ACTI FOLT FOLT
COMPUTER: PC POS/MS-DOS
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Best Local Similarity 54.4%; Pred. No. 0.22
Matches 74; Conservative 0; Mismatches
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,384B
FILING DATE: 05-JUN-95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/966,923
FILING DATE: 27-0CT-1992
APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1993
APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Steeg, Carol Miernicki
REGISTRATION NUMBER: 39,539
REFERENCE/DOCKET NUMBER: 39,539
REFERENCE/DOCKET NUMBER: 01547
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 5011 base pairs
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,384B
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STRANDEDNESS: double
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196..4788
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US-08-461-384B-1
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TELECOMMUNICATION INFORMATION:
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APPLICANT: Orozco, Olivia E.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Fringe Proteins and Pattern Formation
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn Release #1.0, Version #1.30
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APPLICATION NUMBER: 07/966,923
FILING DATE: 27-0CT-1992
APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
APPLICATION NUMBER: 08/141,893
FILING DATE: 26-0CT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Steeg, Carol Miernicki
REGISTRATION NUMBER: 39,539
REFERENCE/DCOKET NUMBER: 01512
TELEPHONE: (613) 545-6853
INFORMATION FOR SEQ ID NO: 1:
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APPLICATION NUMBER: US/08/586,165
FILING DATE: 16-JAN-1996
CLASSIFICATION: 800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08586165
Patent No. 6054298
GENERAL INFORMATION:
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CITY: Lexington
STATE: Massachusetts
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NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                             SEQUENCE CHARACTĒRISTICS:
LENGTH: 5011 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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234 CCGCTCTGGGACTGG 249
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Matches 74; Conservative
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                                                                                                                                                                                                                                                                                                                                                            linear
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; LOCATION: 196.
US-08-407-207A-1
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Human MDR variant
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Nucleotide sequenc
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Human polynucleoti
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Human polynucleoti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T243 gene homologous sequence #1 generated by PCR.
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AAV31498
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   AAS05284 standard; DNA; 471
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 WO200130798-A1.
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Human ORFX ORF790
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | S1DS1/gcgdata/geneseqn-embl/NA1982_DAT:*
| S1DS1/gcgdata/geneseqn-embl/NA1981_DAT:*
| S1DS1/gcgdata/geneseqn-embl/NA1981_DAT:*
| S1DS1/gcgdata/geneseqn-embl/NA1985_DAT:*
| S1DS1/gcgdata/geneseqn-embl/NA1985_DAT:*
| S1DS1/gcgdata/geneseqn-embl/NA1985_DAT:*
| S1DS1/gcgdata/geneseqn-embl/NA1981_DAT:*
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| S1DS1/gcgdata/geneseqn-embl/NA1990_DAT:*
| S1DS1/gcgdata/geneseqn-embl/NA1991_DAT:*
| S1DS1/gcgdata/geneseqn-embl/NA2001_B_DAT:*
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1 acagaaaacaagaaacaaaa.....atggagtccatgtctgagct 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                            1736436 segs, 858457221 residues
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                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    nucleic search, using sw model

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AAX04377
AAS05278
AAS05286
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AAK84729
AAK85983
AAK84730
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match 1
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333.6
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8.4
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66
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39.6
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Perfect :
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The present sequence for T243 homologous sequence #1 is generated by PCR and is homologous to the T243 gene which encodes for a trinucleotide crepeat protein (TRP). The invention describes methods of producing capture (preferably gene T243) encoding a TRP and of target DNA sequence (preferably gene T243) encoding a TRP and of carget DNA sequence (preferably gene T243) encoding a TRP and of producing a knockout mouse comprising a homozygous disruption in a gene concoling TRP, where the disruption inhibits the producing of the wild encoding TRP. The invention also relates to identifying agents cappable of affecting a phenotype of a knockout mouse. Also described are methods of determining whether expansion of the trinucleotide repeat in a gene cocoling TRP produces a phenotypic change. The transgenic animals and the cencelling TRP produces a phenotypic change. The transgenic animals and the calls are useful for identifying compounds capable of ameliorating disease symptoms, and as test substrates for the identification of drugs, disease symptoms, and interventions which may be effective in the training trinucleotide repeat disorders e.g. fragile X syndrome and the training towarders are ideal model systems to study the progression of disease in vivo, the molecular basis of these diseases and show the features observed in human disease. Using the mice, it is possible to model both per progression per per progression per per per progression per per per per pe
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contains heterozygous disruption in a gene encoding TRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 471 BP; 105 A; 129 C; 148 G; 88 T; 1 other;
                                                 Claim 11; Fig 14; 106pp; English.
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24-OCT-2001 (first entry)

AAS21311;

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AAS21244-AAS21518 encode for novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bioactive molecules to calls axpressing PRO polypeptides, and modulate biological activities of cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a call sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or differentiation of chondrocytes, the proliferation or cartilage, the proliferation of inner ear utricular supporting cells or of T-lymphocytes, the release of a cytokine from peripheral blood
                               Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bloactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g. lung, breast, prostate, cervical.
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Z;
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    Human cDNA sequence encoding for PRO4409 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Fig 135; 813pp; English.
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2000WO-US08439.
2000WO-US13705.
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02-JUN-2000; 2000WO-USI5264.
10-NOV-2000; 2000WO-US30873.
                                                                                                                                                                                                                                                                                                                                                                                                                    2000WO-US04341.
2000WO-US04342.
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1E, Goddard A,
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Smith V, Stew
                                                                                                                                             WO200140466-A2.
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11-FEB-2000;
18-FEB-2000;
22-FEB-2000;
24-FEB-2000;
24-FEB-2000;
01-MAR-2000;
20-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-MAY-2000;
22-MAY-2000;
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30-MAR-2000;
                                                                                                                   Homo sapiens.
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Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; limiune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; liflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obsecolast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
 monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adlocytes; or inhibit binding of A-peptide to factor VIIA. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polynuclocides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                               ttgngtcgcccgcgggccttggtcggttcgcaaqccgctagaggtctaccgggcgagggg 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cgggccggagctcgccgttgccgtggttacccagagacacgtgcgcagtcccggaagcgg 376
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                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                         29 ggaaaggactttgccalaggtcgctgaggccaccatctgctctcttactggccaagggcg
                                                                                                                                                                                                 DB 22; Length 1675;
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                                                                                                                                                                                                                                   89; Indels
monocytes (PBMCs), or the proliferation of endothelial
                                                                                                                                          Sequence 1675 BP; 380 A; 469 C; 520 G; 306 T; 0 other;
                                                                                                                                                                                               33.6%; Score 158.2; DB 2
71.3%; Pred. No. 2.1e-35;
ive 0; Mismatches 89
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97US-0049550.
97US-0049606.
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Matches 238; Conservative
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13-JUN-1997;
13-JUN-1997;
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This sequence represents a nucleic acid molecule which encodes a secreted human protein. The gene number, and the clone it is derived from, are detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human mamunoglobulin FC portion (e.g. AAX04302) for increasing the stability of the fused protein as compared to the human protein only.

The invention relates to 86 novel genes and their fragments (nucleic acid sequences: AAX04311-x04410; amino acid sequences AAW78126-W78225) which are useful for preventing, treating or amaliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polymoclecides. Specific uses are described for each of the 86 polymoclecides. Specific uses are described for each of the 86 polymoclecides.
                                                                                                                                                                                                                                                                                                                                               Lafleur DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
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en SM, Shi
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en HS, Rosen CA, Ruben SM,
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                                                                                 97US-0050901.
97US-0052989.
97US-0051919.
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97US-0058668.
97US-0058669.
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970S-0060834
970S-0060841.
970S-0060844.
970S-0060865.
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Ni J, Olsen HS,
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                          97US-0049609.
                                                     97US-0049611.
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P-PSDB; AAW78192.
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           13-JUN-1997;
13-JUN-1997;
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12-SEP-1997;
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02-OCT-1997
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Moore PA,
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Gaps

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Matches 237; Conservative

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197 187 257

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Best Local

127 ggaaaggactttgccataggtcgctgaggccaccatctgctcttactggccaagggcg 186 ggcagtgatatcgctatagggcgccaaagccaccatccgctctctgattgggtgagatgg 196

gaaaaaaaaaaaaaatagttcctctcattggctataaagcagacgagcgaacccattgg taaaaagatag----tcytcccattagctagagagcaaacccc-agaaagcctattgg  ctgcgccgtccgcggggccttggtccgntttgaaggcgggctgcggctgcgagaggagggc 299

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Gaps

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Length 1839; 0; Indels

377

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gene. The T243 gene encodes for a trinucleotide repeat protein (TRP). The invention describes methods of producing embryonic stem (ES) cells comprising a heterozygous disruption in a target DNA sequence (preferably gene T243) encoding a TRP and of producing a Rnockout mouse comprising a homozygous disruption in a gene encoding TRP, where the disruption inhibits the production of the wild type TRP. The invention also relates to identifying agents capable of affecting a phenotype of a knockout mouse. Also described are methods of determining whether expansion of the trinucleotide repeat in a gene encoding TRP produces a phenotypic change. The transgenic animals and the cells are useful for identifying compounds capable of ameliorating disease symptoms, and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel transgenic animals useful as animal model for characterization of function of a gene encoding trinucleotide repeat proteins (TRPs), contains heterozygous disruption in a gene encoding TRP -
                                                                                                                                                                                                                   The present sequence represents the DNA sequence of an expanded T243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trinucleotide repeat protein; TRP; T243; embryonic stem cell; ES; transgenic animal; knockout mouse; triplet repeat expansion; fragile X syndrome; Huntington's disease; mouse; mutant; ds.
                                               Sequence 1839 BP; 424 A; 522 C; 535 G; 358 T; 0 other;
the trinucleotide repeat instability in the mouse.
                                                                                                                     14.0%; Score 66; DB 22; 1
100.0%; Pred. No. 5.6e-09;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= a
/product= "Expanded TRP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA sequence of an expanded T243 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 15; 106pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAS05286 standard; DNA; 1848 BP.
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                                                                                                                                               Best Local Similarity 100.
Matches 66; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (DELT-) DELTAGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-300473/31.
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                                                                                                                                                                                                                                                                                                                            466 tgagct 471
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAS05286;
                                                                                                                             Query Match
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(TRP). The invention describes methods of producing embryonic stem (ES)

cells comprising a heterozygous disruption in a target DNA sequence

(preferably gene T44) encoding a TRP and of producing a knockout mouse

comprising a homozygous disruption in a gene encoding TRP. Where the

disruption inhibits the production of the wild type TRP. The invention

also relates to identifying agents capable of affecting a phenotype of

a knockout mouse. Also described are methods of determining whether

ca knockout mouse. Also described are methods of determining whether

ca knockout mouse. The transgenic animals and the cells are useful for

chentifying compounds capable of ameliorating disease symptoms, and as

cherapies and interventions which may be effective in treating.

cherapies and interventions which may be effective in treating of disease. The animal models for trinucleotide repeat disorders e.g. fragile X syndrome and Huntington's

chincelotide repeat disorders e.g. fragile X syndrome and Huntington's

chincelotide repeat disorders e.g. fragile X syndrome and Huntington's

disease. The animal models for trinucleotide repeat disorders are ideal

model systems to study the progression of disease in vivo, the molecular

basis of these diseases and show the features observed in human disease.

Using the mice, it is possible to model both the pathogenic mechanism and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel transgenic animals useful as animal model for characterization of function of a gene encoding trinucleotide repeat proteins (TRPs), contains heterozygous disruption in a gene encoding TRP -
                            ccgggggaagctgctccgcgcgcgcgcggaggaagcgccgccgggtccgctctgctct 436
                                                                                                                                                    cgggccggagctcgccgttgcccgtggttacccagagacacgtgcgcagtcccggaagcgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Trinucleotide repeat protein; TRP; T243; embryonic stem cell; ES; transgenic animal; knockout mouse; triplet repeat expansion; fragile X syndrome; Huntington's disease; mouse; murine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murine trinucleotide repeat protein (TRP) cDNA sequence.
                                                                                                                                                                                                      gggtccggctgggccatggagtccatgtctgagc 470
                                                                                                                                                                                                                                   Moore M, Allen KD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                AAS05278 standard; cDNA; 1839 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "TRP"
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04-FEB-2000;
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test substrates for the identification of drugs, pharmaceuticals, therapies and interventions which may be effective in treating trinucleotide repeat disorders e.g. fragile X synforme and Huttington's disease. The animal models for trinucleotide repeat disorders are ideal model systems to study the progression of disease in vivo, the molecular basis of these diseases and show the features observed in human disease. Using the mice, it is possible to model both the pathogenic mechanism and the trinucleotide repeat instability in the mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; antitivation; antitivation; antitivation; antidiabetic; antitivation; antitivation; antitioneantic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; severe combined immunodeficiency; anticimmune disorder; asthma; allery; aplastic anaemia; nocturnal haemoglobinitia; burn; wound;

    36 ggaggaagcgccgcgcgctctgctctggtccggctgggccatggagtccatgtc 465
    36 ggaggaagcgccgcgggtccgctctgctctggtccggctgggccatggagtccatgtc 68
    37 ggaggaagcgccgggtccgctctgctctggtccggctgggccatggagtccatgtc 68

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                                                                                                                                                                                               Gaps
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0
                                                                                                                                                                   Length 1848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human ORFX ORF790 polynucleotide sequence SEQ ID NO:1579.
                                                                                                                                                                                             Indels
                                                                                                                          Sequence 1848 BP; 415 A; 519 C; 543 G; 371 T; 0 other;
                                                                                                                                                               Query Match 14.0%; Score 66; DB 22; L. Best Local Similarity 100.0%; Pred. No. 5.6e-09; Matches 66; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                     AAC75235 standard; cDNA; 2829 BP
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99US-0127636.
99US-0127728.
2000US-0540763.
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05-APR-1999;
30-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                          08-FEB-2001
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                                                              AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: oytostatic; hepatorropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          coagulation; to inhibit thrombosis; and as a contraceptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2829 BP; 799 A; 585 C; 692 G; 752 T; 1 other;
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Pred. No. 0.002;
0; Mismatches 113;
Claim 5; Page 1281-1283; 5507pp; English.
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2000US-0184664
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Best Local Similarity 50.2
Matches 114; Conservative
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| 000US - 0186350<br>000US - 0189874<br>000US - 01998123<br>000US - 0205515<br>000US - 020467<br>000US - 0215138<br>000US - 0216880<br>000US - 0217447<br>000US - 0217487<br>000US - 0217487  | 000005-0224518<br>000005-0225218<br>000005-0225218<br>000005-0225268<br>000005-0225268<br>000005-0225268<br>000005-0225757<br>000005-0225757<br>000005-0225758<br>000005-0225758<br>000005-0225758<br>000005-0225758<br>000005-0225758<br>000005-0225758<br>000005-0225758<br>000005-0225758   | 20000S-0231244. 20000S-0231413. 20000S-0231413. 20000S-023281414. 20000S-0232814. 20000S-023299. 20000S-023299. 20000S-023299. 20000S-023299. 20000S-0232400. 20000S-0232400. 20000S-0232400. 20000S-0232400. 20000S-0232400. 20000S-0233884. 20000S-0238886. |
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(HUMA-) HUMAN GENOME SCI INC.

Ruben Barash SC, Rosen CA,

SM

WPI; 2001-483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -

Disclosure; SEQ ID NO 39541; 3071pp + Sequence Listing; English.

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4-SEP-2000
             AMM64951 to AAM64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased that affect the activity of (I) by expressing in activity of (I) by expressing inactive proteins or to cylonucleotides may be used to product the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the classos and treat immune/haematopoletic-related diseases, especially cancers and cancer metastases of haematopoletic-derived cells. AAM64703 cancers and cancer metastases of haematopoletic-derived genomic sequences from the present invention. AAM54942 to AAM54950 and AAM82169 crepresent sequences used in the exemplification of the present invention.
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ID AAK85983 standard; DNA; 48037 BP.
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AMK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polymucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and matastasis.
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2000US-0249297.
2000US-0249299.
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that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic actived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'Human; immune; haemaţopoietic; immune/haematopoietic antigen; cancer;
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                                                                                                                                                          Sequence 48037 BP; 12892 A; 9814 C; 10466 G; 14865 T; 0 other;
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02-OCT-2000;
02-OCT-2000;
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02-0CT-2000;
02-0CT-2000;
13-0CT-2000;
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20-0CT-2000;
20-0CT-2000;
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27-SEP-2000;
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2000US-0246524.
2000US-0246525.
2000US-0246527.
2000US-0246527.
2000US-0246632.
2000US-0246610.
2000US-0246611.
2000US-0246611.
2000US-0246611.
2000US-0246611.
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2000US - 0249211.
2000US - 0249213.
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2000US - 0249214.
2000US - 0249215.
2000US - 0249216.
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2000US-0251856.
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2000US-0251869.
2000US-0251989.
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17-NOV-2000;
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(HUMA-) HUMAN GENOME SCI INC

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -

Disclosure; SEQ ID NO 39542; 3071pp + Sequence Listing; English

AAK54951 to AAK64702 encode the human immune/haematopoletic antigen (I)
amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
cypression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
coplanded may be used to produce the secreted (I), by inserting
the nucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
diagnose and treat immune/haematopoletic-related diseases, especially
cancers and cancer metastases of haematopoletic-derived cells. AAK64703

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08-NOV-2000;
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to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                            325 agottogocogttgccogtgottacccagagacacgtgcgcagtcccggaagcggccggggga 384
                                                                                                                                                                                                300 GCTGCTCCCGCCGCCGCCGCCGCCGCCGCCCCCCCCGGATCCATGATCGG 241
                                                                                                                                                                                                                                                                                                                                                                                                                           Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40796
                                                                                                       0; Gaps
                                                                                                                                                                                                                          385 agctgctccgcgcgcgcgctgccggaggaagcgccgccgggtccgctctgctctgggtccgg
                                                                              Ouery Match 8.4%; Score 39.6; DB 22; Length 48045; Best Local Similarity 50.5%; Pred. No. 0.61; Matches 96; Conservative 0; Mismatches 94; Indels 0;
                                            Sequence 48045 BP; 12889 A; 9812 C; 10461 G; 14883 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                       AAK85984 standard; DNA; 48045 BP
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2000US-0180628.
2000US-018664.
2000US-0189374.
2000US-0189874.
2000US-0199123.
2000US-020515.
2000US-020515.
2000US-020515.
2000US-020515.
2000US-020515.
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2000US-0217487.
2000US-0217496.
2000US-0218290.
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2000US-0220964
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2000US-0224519
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                                                                                                                                                                                                                                                                                          240 GGGGCCGTG 231
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16-MAR-2000; 2
18-MAR-2000; 2
19-MAY-2000; 2
07-JUN-2000; 2
30-JUN-2000; 3
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07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
14-JUL-2000;
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26-JUL-2000;
14-AUG-2000;
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PR 14-ANG-2000, 2000US-022540.

PR 14-ANG-2000, 2000US-022540.

PR 14-ANG-2000, 2000US-022541.

PR 14-ANG-2000, 2000US-022547.

PR 14-ANG-2000, 2000US-0225759.

PR 14-ANG-2000, 2000US-0225759.

PR 14-ANG-2000, 2000US-0225759.

PR 18-ANG-2000, 2000US-0225759.

PR 18-ANG-2000, 2000US-0225759.

PR 22-ANG-2000, 2000US-0225769.

PR 22-ANG-2000, 2000US-0225769.

PR 22-ANG-2000, 2000US-0225769.

PR 22-ANG-2000, 2000US-022944.

PR 01-SEP-2000, 2000US-023944.

PR 01-SEP-2000, 2000US-023944.

PR 01-SEP-2000, 2000US-023944.

PR 14-SEP-2000, 2000US-023994.

PR 14-SEP-2000, 2000US-023994.

PR 14-SEP-2000, 2000US-023994.

PR 29-SEP-2000, 2000US-023994.

PR 29-SEP-2000, 2000US-023994.

PR 29-SEP-2000, 2000US-023994.

PR 29-SEP-2000, 2000US-023994.

PR 20-CCT-2000, 2000US-023994.

PR 20-CCT-2000, 2000US-0241787.

PR 20-CCT-2000, 2000US-024617.

PR 20-CCT-2
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Ruben SM
      2000US-0246528.
2000US-0246692.
2000US-0246610.
2000US-0246611.
2000US-0246613.
2000US-0249203.
2000US-0249209.
2000US-0249209.
                                                              2000US-0249211.
2000US-0249212.
2000US-0249213.
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2000US-0249265.
2000US-0249297.
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2000US-0251479.
2000US-0251856.
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                                                                                                      20000S-0249218
20000S-0249244
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               08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
                                 08-NOV-2000;
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WPI; 2001-483426/52

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis metastasis

Disclosure; SEQ ID NO 40796; 3071pp + Sequence Listing; English.

AMK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased content affect the activity of (I) by expressing inaptient's genome that affect the activity of (I) by expressing inactive proteins or to plynucleotides may be used to production of (I). Additionally, (I) collynicationally (I) and applement the patients own production of (I). Additionally, (I) the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent. (C) protein (I) proteins and polynucleotides may be used to prevent. (I) adamone and treat immune/haematopoietic-derived cells. AAK64703 cancers and cancer metastases of haematopoietic-derived cells. AAK64703 cancers and cancer metastases of haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 ceptessent sequences used in the exemplification of the present invention.

Sequence 48045 BP; 12889 A; 9812 C; 10461 G; 14883 T; 0 other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC98773 to AAC99231 encode the human pancreatic cancer associated proteins, called pancreatic cancer antigens, given in AAB54008 to AAB54466. The human pancreatic cancer antigens have cytostatic. neuroprotective, nootropic, immunomodulatory, relaxant, contraceptive, gynaecological, cardiant and antiinflammatory activities, and can be used for greenting, treating, or amaliorating a medical condition or in assays for diagnosing a pathological condition or a susceptibility to one in a subject. Binding partners to the proteins and the activity of the proteins can be used for detect, iteat or prevent pancreatic cancer antigens can be used to detect, treat or prevent pancreatic disorders, especially cancer.
                                                                                               361
                                                                                                                                                                                                               300 GCTGCTCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCGATCCATGATCG 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  detection; diagnosis; identification; cytostatic; neuroprofective; nootropic; immunomodulatory; relaxant; contraceptive; gynaecological; antiinflammancry; cardiant; gene therapy; chromosome mapping; linkage analysis; tissue identification; tissue typing; forensic; neural; immune system; muscular; reproductive; gastrointestinal; pulmonary; cardiovascular; renal; proliferative; ss.
                                                                                                                                                                301
                                                                                                                                                                                         385 agctgctccgcgcgctgccggaggaagcgccgccggtccgctctgctctgggtccgg 444
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid that is a pancreatic cancer antigen for preventing, treating, or ameliorating a medical condition, particular pancreatic cancer, or for use in assays for diagnosing a pathological condition
                                                                                                                          325 agctcgccgttgccgtggttacccagagacacgtgcgcagtcccggaagcggcggggg
                                                                                                                                              Human pancreatic cancer antigen nucleotide sequence SEQ ID NO:272.
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   Length 48045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pancreatic cancer; pancreatic cancer antigen;
                                  Indels
                              94;
 DB 22;
 Score 39.6; DB
Pred. No. 0.61;
                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 708; 1379pp; English.
                                                                                                                                                                                                                                                                                                                                                                            BP.
                                                                                                                                                                                                                                                                                                                                     RESULT 11
AAC99044/c
ID AAC99044 standard; cDNA; 527
 8.48;
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                            96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rosen CA, Ruben SM;
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                                                                                                                                                                                                                                                                                        240 GGGGCCGTG 231
               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; pancreas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAB54279
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Query Match
                 Best Local
                              Matches
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Agonists and antagonists to the antigens can be used to design nucleic pancreatic cancer antigen polynucleotides can be used to design nucleic acid hypitdisation probes that can be used in chromosome mapping, linkage analysis, tissue identification and/or typing and avariety of forensic and diagnostic methods. The proteins can be used to generate antibodies which are used to purity, detect and target the polypeptides, including both in vivo and in vitro diagnostic and therapeutic methods. The proteins can be used to treat or prevent neural, immune system, muscular, responductive, gastrointestinal, pulmonary, cardiovascular, renal or proliferative disorders. AAC99212 to AAC99240 and AAB54467 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antisense oligonucleotides, useful for treatment and prevention of hypertension and myocardial ischemia, are directed against mRNA encoding the betal-adrenoceptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention provides a composition comprising at least one oligonucleotide, of 9-35 bases, that binds specifically to part of the
                                                                                                                                                                                                                                                                                                                                                                                                                                      269 GCTGCTCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGATCCATGATCGG 210
                                                                                                                                                                                                                                                                                                                          325 agetegeegttgeegttgetacceagagacacgtgegeagteeeggaageggeggggg 384
                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypertension; canine; ds.
                                                                                                                                                                                                                                                                                                                                                                               ó
                                                                                                                                                                                                                                  Score 39.2; DB 21; Length 527; Pred. No. 0.17;
                                                                                                                                                                                        Sequence 527 BP; 58 A; 206 C; 184 G; 74 T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Canine betal-adrenoceptor polynucleotide sequence
                                                                                                                                                                                                                                                                   94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Betal-adrenoceptor; antisense; transcription; myocardial ischemia; hypotensive; vasotropic;
                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 4; Page 90-91; 144pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
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                                                                                                                                                                                                                                       8.3%;
50.0%;
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                                                                                                                                                                                                                                                                      95; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYFL ) UNIV FLORIDA.
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                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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polypeptide. Binding of the oligo to the betal-adrenoceptor mRNA, expressed from the gene encoding a mammalian betal-adrenoceptor mRNA alters transcription of the mRNA in cells. The compositions are used to treat diseases associated with increased number or activity of the cliseases associated with increased number or activity of the cliseases associated with increased number or activity of the cappositions can also be used to produce recombinant (viral) vectors for use in vaccines, for treating or preventing the diseases. The antisense oligos may also be used to detect the mRNA or related DNA, including visualization within a cell, to generate transgenic animals with altered betal-adrenoceptor activity, and to screen patients for susceptibility to hypertension, by detection of particular alleles of betal-adrenoceptor genes. The present sequence represents the polynucleotide sequence of the canine betal-adrenoceptor (GenBank Acon No: U73207).
                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzhaimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     258 gregececegadercecedecegercadecaccececececececedeageared 199
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                                                                                                                                                                                                                                                                                                                                                                                                                        Ren F, W
Zhang J;
                                                                                                                                                                                                                                                                                           Length 1845;
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Yang Y,
                                                                                                                                                                                                                                          Sequence 1845 BP; 197 A; 754 C; 647 G; 246 T; 1 other;
                                                                                                                                                                                                                                                                                               DB 21;
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Xue AJ,
                                                                                                                                                                                                                                                                                                              0.3;
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                                                                                                                                                                                                                                                                                             Score 39;
Pred. No. 0
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Wehrman T,
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2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
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2000US-0693036
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                                                                                                                                                                                                                                                                                                                                86; Conservative
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                                                                                                                                                                                                                                                                                                                Similarity
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Tang Z,
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19-JUL-2000;
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14-SEP-2000;
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25-APR-2000;
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Wang J,
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Best Local S
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Xu C,

Wang

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AA158570 standard; cDNA; 3577 BP.
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     WPI; 2001-442253/47.
P-PSDB; AAM41200.
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                                                                                                                                      tg 432
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                                                                                       Query Match
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                                                                                                                                      431
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Zhao QA,
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Wang J,
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                                                                                                                                                                 The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM36642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide system, such as peripheral nervous injuries, peripheral nervous system auch as peripheral nervous injuries, peripheral nervous localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic atteral scierosis, and Shy-Drager Syndrome. Other uses include the Activiriation of the activities such as: Immune system suppression, and thrombolytic activity, chemoclactic/chemoclinetic activity, haemostatic assays for receptor activity, arthritis and inflammation, leukaemias and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human: nootropic: immunosuppressant; cytostatic; gene therapy; cancer;
peripheral nervous system; neuropathy; central nervous system; CNS;
Alzheimer's: Parkinson's disease; Huntington's disease; haemostatic;
amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    311 gaggggcggggccggagctcgccgttgccgtggttacccagagacacgtgcgcagtccgg 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     356 CTTTAGTGGTGTCATGCCGCCGAGCACTTCGTCCTGGTCGTCCTGGGGAGCAGCACCAC 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     296 GTTGGGCCTCCGGGTTCCCGCAGCCACCCGAAGACCCCCAGGCAGCCGCCCAGCACCAG 237
                                                                                 Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries \boldsymbol{\cdot}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match
B.2%; Score 38.6; DB 22;
Local Similarity 50.5%; Pred. No. 0.49;
les 92; Conservative 0; Mismatches 90;
       RT;
                                                                                                                                Claim 1; SEQ ID NO 4345; 10078pp; English.
   Drmanac
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   Goodrich R,
Zhao QA, Zhou P,
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous to factual sed neuropaths and central nervous system diseases, such as lateral solerosis, and Shy-Drager Evoluce, Other uses include the utilisation of the activities such as: Immune system suppression, and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic assays for receptor activity, arthritis and inflammation, leukaemias and includers.
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                                                                                                                                                                                                                                                                                                                   Ren F, W.
Zhang J;
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Yang Y,
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Xu C, Xue AJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 773; 10078pp; English.
                                                                                                                                                                                                                                                                                                         Asundi V, Che
Wehrman T, Xu
Goodrich R,
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                                        21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-055317.
09-JUL-2000; 2000US-058042.
19-JUL-2000; 2000US-0620312.
03-AUC-2000; 2000US-0653450.
14-SEP-2000; 2000US-0653191.
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2000WO-US34263
                                                                                                                                                                                                             2000US-0727344
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Matches 92; Conservative
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Wang Z, W
Zhou P,
                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC.
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P-PSDB; AAM39414
                                                                                                                                                           14-SEP-2000; 219-OCT-2000; 29-NOV-2000; 2
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26-DEC-2000;
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Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss
                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess blodiversity -
            DNA encoding novel human diagnostic protein #20510.
                                                                                                                                                                                                                                                         Claim 1; SEQ ID No 20510; 103pp; English
                                                                                                                                                                       Tang YT;
                                                                                                                            31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                             30-MAR-2001; 2001WO-US08631.
13-FEB-2002 (first entry)
                                                                                                                                                                       Drmanac RT, Liu C,
                                                                                                                                                                                        WPI; 2001-639362/73
                                                                                                                                                       (HYSE-) HYSEQ INC
                                                                                                                                                                                                 P-PSDB; ABG20519
                                                                          WO200175067-A2.
                                                            Homo sapiens.
                                                                                             11-OCT-2001
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The invention relates to isolated polynucleotide (I) and polynerase chain reaction (FOR) primers, oligomers, and for chromosome polymerase chain reaction (FOR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The and gene mapping, and in recombinant production of (II). The chromosome polynucleotides are also used in diagnostics as expressed sequence tags polynucleotides are also used in fagnes therapy techniques for reactors normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical clasorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in and to produce other types of data and products dependent on DNA and among acid sequences. AAS64197-AAS94564 represent novel human can diagnostic coding sequences of the invention.

Specification, but was obtained in electronic format directly from WIPO specification, but was obtained in electronic format directly from WIPO at fire invention.
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pred. No. 0.49;
0; Mismatches 90;
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nes 92; Conservative
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Matches
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δλ qq δλ ДQ ò qq

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176 TG 175
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431 tg 432

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Search completed: May 24, 2002, 00:24:32 Job time: 9089 sec

Searched:

Run on:

Database

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ACUTAZU 89855 bp DNA linear HTG 25-JAN-2002 Mus musculus chromosome 17 clone RP23-76116 strain C57BL6/J, WORKING DRAFT SEQUENCE, 38 unordered pieces.
                                      3549 Mus muscu
1644 Mus muscu
898 Homo sapi
961 Homo sapi
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6 Homo sapi.
9 Homo sapi.
2 Homo sapi.
8 Homo sapi.
Rattus norv.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 8985)
Han, J., Montgomery, K.T., Grills, G., Lee, E., Long, J., Pomerantz, R.,
Ioshikhes, I.P., Shim, C., Decker, J., Thomas, E., Perera, A.,
Gordon, M., Goltz, J. S. and Kucherlapati, R.
High Throughput Mouse Sequencing
                                                                                                                                    Mus muscu
Rattus no
Pan trogl
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Rattus no
Homo sapi
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Han,J., Montgomery,K.T., Grills,G., Lee,E., Long,J., Pomerantz,R.,
Ioshikhes,T.P., Shim,C., Decker,J., Thomas,E., Perera,A.,
Gordon,M., Goltz,J.S. and Kucherlapati,R.
Direct Submission
 AC074220 Mus muscu
BC004423 Homo sap1
AL035587 Human DNA
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Mus muscu
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AUTHORS
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                                                         May 24, 2002, 00:14:24 ; Search time 3953.4 Seconds (without alignments) 2493.145 Million cell updates/sec
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    GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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TITLE

Description

Score

Result No.

JOURNAL

COMMENT

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ocontig of 1001 bp in length is gap of unknown length contig of 1417 bp in length gap of unknown length length is contig of 749 bp in length gap of unknown length contig of 859 bp in length.
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of 1817 bp in length
              unknown length
of 1529 bp in length
unknown length
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of 1223 bp in length
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27098. .28819
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/note="assembly_name:Contig137"
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of 1311 bp
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/organism="Mus musculus"
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                                                                                               http://wchanning.bwh.harvard.edu:9088/hpcgg/jsp/hpcgg/Sequence/mous
e.html
Submitted (20-JUL-2000) Department of Molecular Genetics, Albert Einstein College of Medicine Genome Center, 1300 Morris Park Ave. Bronx, NY 10461, USA On Apr 28, 2001 this sequence version replaced gi:11276104.
                                                                                                                                                                                                                                                                       Quality coverage: agarose-FP - N/A Quality coverage: 5.1 x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 38 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                Center project name: ADY
Sequencing vector: p0C18; L08752
Sequencing vector: p0C18; L08752
Chemistry: Dye-terminator Big Dye; 1008
*Consensus quality: 79355 at least Q20
*Consensus quality: 69022 at least Q40
Estimated insert size: agarose-FP - N/A
*Estinated insert size: 89115 - sum-of-contigs
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of 2335 bp in length
unknown length
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gap of unknown length
contig of 5942 bp in length
gap of unknown length
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gap of unknown length
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of 2909 bp in length
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 9 Row: o Column: 7
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 5729791.

1. 1720
/ Organism-"Homo sapiens"
/ Obsaref-"Homo sapiens"
/ Clone-"MGC:3530 IMAGE:2819660"
/ Clissue-"MGC:3530 IMAGE:2819660"
/ Clone-"MGC:3530 IMAGE:281960"
/ Lissue-Lype-"Lung, mail cell carcinoma"
/ Lissue-Lype-"Lung, mail cell carcinoma"
/ Lissue-Lype-"Lung, mail cell carcinoma"
          BC004423 1720 bp mRNA linear PRI 12-JUL-2001
Homo sapiens, clone MGC:3530 IMAGE:2819660, mRNA, complete cds.
BC004423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /Translation-"MOSMPEPASRCILLILPLILLLLILPAPELGPSOAGABENDWVR
IDPSKCEVCKYVAVELKSAFEETGKTKEVIGTGYGILDOKASGVKYTKSDLRLIEVTET
ICRRLLDVSTAKBATGSNFRAKGWSETFETLINLVHKGVKVWYNDIPYELWBETSBEV
DLKKQCDVLVPEFEETGY IDWYRNHQEEDLTEFLCANIVLKGKDTSCLAEOWSGKKGDY
AALGGKKSKKKSSRAKAAGGRSSSSKQRKELGGLEGDPSPEEDEGIQKASPLTHSPPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Stanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeayy, Steven Ses, Pawan Pandoh, Anna-Lisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smallus, Michael Smith, Lorraine Spance, Jeff Stott, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra
                                                                                                                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                      Direct Submission
Submitted (12-MAR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ggcagtgatatcgctatagggcgccaaagccaccatccgctctctgattgggtgagatgg 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="Unknown (protein for MGC:3530)"
/protein_id="AAH04423.1"
/db_xref="GI:13325208"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Pred. No. 9.9e-27;
0; Mismatches 88
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388. .1224
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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                                                                        BC004423.1 GI:13325207
                                                                                                                                                                                                                                                                                                                                                               Contact: MGC help desk
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Strausberg, R.
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Best Local Similarity 71.6%;
Matches 239; Conservative (
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                                                                                                                   human,
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DEFINITION
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                                                                                                                                 ORGANISM
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AUTHORS
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ORIGIN
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                                                                          foote-massembly_name:Contigl27"
foote-massembly_name:Contigl27"
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foote-massembly_name:Contigl26"
foote-massembly_name:Contigl24"
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foote-massembly_name:Contigl27"
foote-massembly_name:Contigl19"
foote-massembly_name:Contigl18"
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                 /note="assembly_name:Contigl29"
58870. .60621
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60642. .62255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79257. 81332
/note="assembly_name:Contig115"
81353. 83169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.9%; Score 451.6; DB 2
llarity 98.7%; Pred. No. 7.7e-94;
Conservative 0; Mismatches 5
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Best Local Similarity
Matches 465; Conserv
misc_feature
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The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw., SWISSPROT; Tr:, TREMBL; Wp:, WORNEP; Information on the WORNEPE database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6 Pound at Park Cancer institute by the group of pieter de Jong. For further park Cancer institute by the group of pieter de Jong. For further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HS475N16
Human DNA sequence from clone RP3-475N16 on chromosome 6pl2.3-21.2.
Contains the genes for CTG4A, pre-T cell receptor alpha, a novel protein similar to RP17A (60S ribosomal protein L7A) and the 3' end gene KIAA0240. Contains ESTs, STSs, GSSs and four putative CpG islands, complete sequence.
AL035S87 5 GI:6002306
HTG: CpG island; CTG4A; KIAA0240; RPL7A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 113109)
Williams, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (02-FEB-2000) Sanger Centre, Hinxton, Cambridgeshire,
CBL0 15A, UR. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
on Sep 30, 1999 this sequence version replaced gi:5921383.
                                                                                                                                                                                               140 TAAAAAGATAG-----TCCTCCCATTAGCTAGAGAGCAAACCCC-AGAAAGCTATTGG 192
                                                                                        193 CTGCGCCGTCCGCGGGCCTTGGTTTGAAGGCGGGCTGCGGCTGCGAGGAGGGGC 252
                                                          257 ttgngtcgccgcggggccttggtcggtttcgcaagccgctagaggctaccgggcgaggg
                                                                                                                                                                       317 cgggccggagctcgccgttgccgtggttacccagagacacgtgcgcagtcccggaagcgg
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                              gggtccggctgggccatggagtccatgtctgagc 470
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/db_xref="taxon:9606"
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HS475N16/c
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Em:AA70232 Em:A1413153 Em:A404894 Em:A1902140
Em:AA712406 Em:A1391065 Em:A1464828 Em:N31024 Em:W29254
Em:AA772406 Em:AA68594 Em:AA292739 Em:C18340
Em:AA7124002 Em:R469640 Em:T66538 Em:A3718500 Em:AW007167
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Em:A55954 Em:AA492Em:A33844674 Em:AA19760
Em:AA57832 Em:AA4467 Em:A3384656263 Em:A1386455 Em:A1838465 Em:A1356413
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DLKKQCDVLVPEFEFETGSNRFAGGREFFETGTHNLVHKGKDTSCLAFQWSGKKGDT
AALGGKKSKKKSSRAKAAGGGRSSSSSKQRKELGGLEGDPSPFEDGGIQKASPLTHSPPD
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/gene="dJ475N16.1"
/note="owing to a frameshift at 15781 compared to CDNA em:U80744 our translation differs considerably from the published tr:015412 protein, adding two more coding exons to 3' or C terminal end; match: proteins: Tr:015412"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(12117. 12836,13197. 13314,13565. 13687,
15734. 15830,16806. 16929,21683. 22204))
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note="LIMA4A repeat: matches 6197. .6277 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                          5844 . 6032
/note="Tigger2a repeat: matches 4. .216 of consensus"
6563 . 6699
                                                           /note="MER51B repeat: matches 504. .617 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7000. 7061
/note="MER91B repeat: matches 91. .157 of consensus"
Anote="FLAM_C repeat: matches 1. .133 of consensus"
84455. .8949
/note="FLAM_C repeat: matches 2. .133 of consensus"
10905-.11215
/note="Anusgi repeat: matches 1. .309 of consensus"
complement(12117. .22204)
/gene="dJ478N16.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="MER91B repeat: matches 1. .123 of consensus"
'note="Alu repeat: matches 1. .70 of consensus"
                                                                                                                                                                                                                                                                369 of
                                                                                                                                                                                                                                                                                                              476. .5525
hote="Tigger2a repeat: matches 246. .299 of
                                                                                                                                                                                                    .444 of
                                                                                                                                                                            4703. .4772
/note="Tigger2a repeat: matches 369.
5085. .5180
                                                                                                                                                                                                                                /evidence=not_experimental
/product="dJ475N16.1 (CTG4A)"
/protein_id="CAB75301.1"
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/gene="dJ475N16.1"
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PRI 18-DEC-1997
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LPSRCEVCKYVAVELKSAFEETGKTKEVIGTGYGILDOKASGVKYTKSDLRLEVTET
ICKRLLIIACTRRGPAAIDLPRACQRPLRHYTTWYTKGSRW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Journal Logical Logical Margolis, R.L., S.H., Kidwal, A.S., Margolis, R.L., Abraham, M.R., Gatchell, S.B., Ll, S.H., Kidwal, A.S., Breschel, T.S., Silne, O.C., Callahan, C., McInnis, M.G. and Ross, C.A. Direct Submitted (02-DEC-1996) Psychiatry, Johns Hopkins Univ. Sch. of Med., 600 N. Wolfe Street, Meyer 2-181, Baltimore, MD 21205, USA L. 962 / Organism="Homo saplens" / Organism="Homo saplens" / Organism="Homo saplens" / Chromosome="1" / Chrom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Margolis, R.L., Abraham, M.R., Gatchell, S.B., Li, S.H., Kidwal, A.S., Breschel, T.S., Stine, O.C., Callahan, C., Mcinnis, M.G. and Ross, C.A. CDNAs with long CAG trinucleotide repeats from human brain Hum. Genet. 100 (1), 114-122 (1997)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 962)
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                                                                                                                                                                                                                                                                                                                                                    22081 TAAAAAGATAG-----TCTTCCCATTAGCTAGAGAGAAAAC-CCCAGAAAAGCTATTGG 22029
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                                                                                                                                                                                                                                                                                                                       317 cgggccggagctcgccgttgccgtggttacccagagacacgtgcgcagtcccggaagcgg
                                                                                                                     Length 113109;
                                                                                                                                                                        Indels
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                                        conserved
                                                                                                    Query Match 33.6%; Score 158.2; DB 9; Best Local Similarity 71.3%; Pred. No. 2.6e-26; Matches 238; Conservative 0; Mismatches 89;
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Homo sapiens CTG4a mRNA, complete cds.
U80744
                            /note="21 copies 2 mer ac 90% 41779. .41844
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/db_xref="G1:2565063"
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388. .819
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/gene="CTG4a"
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/gene="dJ475N5.2"
/chote="match: CDNAs: Em:U16958 Em:U36759 Em:U38996; match: ESTS: Em:AA913164 Em:A1263200 Em:A1285999 Em:AW014894
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/evidence=not_experimental
complement(25571. 336438)
/gene="dJ475N16.2"
/gene="dJ475N16.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MAGTWILLILALGCPALPTGVGGTPFFSLAPPIMLLVDGKQQWVVCLVLDVAPPGLDSPIWFSAGNGSALDAFTYGPSPATDGTWTNLAHLSLPSBELASW BEPLCHTGPOAEGHSRSTOPWHILSGENSTARTCPQPPLRGGGGLLRAPERFLLAGTPG GALWLGVLRLLIFVLLLFDLLTGSCLCDPAGPLPSPATTTRLRALGSHRLHPATETG GREATSSPRPQPRDRRWGDTPPGRKPGSPVWGEGSYLSSYPTCPAQAWCSRSALRAPSSLGAFFAGDLPPPLQAGAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="dJ475N16.2"
complement(join(25571. .26188,27131. .27175,28057. .28377,
35277. .35438))
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35277. .35334))
/gene="dJ475N16.2"
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/note="Alusc repeat: matches 1. .306 of consensus"
/note="LIMB8 repeat: matches 6101. .6170 of consensus"
33433. .33494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="LiMB3 repeat: matches 6024. .6137 of consensus" 38610. .38858 //note="LiMB3 repeat: matches 5711. .6024 of consensus" 38941. .39002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38941, 39002
/note="Aluj/FLAM repeat: matches 19, .80 of consensus"
39289, 39862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .5817 of consensus"
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/db_xref="G1:6969164"
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21516. .22025
/note="CpG island"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="31 copies 2 mer tt 69% conserved"
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0745. .40851
/note-"LIP4 repeat: matches 5703.
41336. .4137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         matches 2.
                                                                                                                                                                                      21749. .21784
//note="match: STS: Em:AF021121"
complement(21753. .21788)
/gene="d3475N16.1"
                                                                                                                                                                                                                                                                                             /note="match: STS: Em:G09564"
21759. 21794
/note="match: STS: Em:Z67474"
21762. 21797
/note="match: STS: Em:G09799"
complement(21762. 21793)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(23719 23975)
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complement(24876 25553)
/note="match: GSS: Em:AQ383009"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complemen((22138, .22473))
/note="match: GSS: Em:A0756680"
23412, .23718
/note="AluSc repeat: matches 2.
/note="match: STS: Em:G37319"
complement(17091. .17133)
/gene="dJ475N16.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="match: STS: Em:G09544" complement(22138, .22473)
                                                                                                                                                             /evidence-not_experimental
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BASE COUNT ORIGIN

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CE 2 (bases 1 to 1909)

RS Glozak,M.A., Li,Y., Reullle,R. and Rogers,M.B.

Blirect Submission

L Submitted (15-MAR-2001) Biology, University of South Florida, 4202

E. Fowler Avenue, Tampa, FL 33620, USA

Location/Qualifiers

1. 1909

Ab_xref='taxon:10090"

//cell_line='#Ryl9; derived from matings between C3H/He
females and male animals carrying an X chromosome derived
from a feral mouse (McBurney & Rogers, Dev. Biol., 89,
503)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cell_type="embryonal carcinoma"
/clone_lib="24 hr retinoic acid-treated P19 cDNA (Bouillet
et al. Dev. Biol., 170, 420)"
89. 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF361644 1909 bp mRNA linear ROD 12-MAY-2001 Mus musculus putative retinoic acid-regulated protein mRNA, complete cds.
                                                                                                                                                                                                                                                                        /product="Riken cDNA 1600025D17 gene"
/product="Riken cDNA 1600025D17 gene"
/product="15488B148"-11.
/product="154888"-11.
/product="15488B148"-11.
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/product="15488B148"-11
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                                                                                                            month old male mouse."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/product="putative retinoic acid-regulated protein"
/protein_id="AAK52494.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1882,
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                                    /db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="mgC=19340 IMAGE:4222133"
/tissue_type="Kidney, normal.5 m
/clone_lib="NcI_CGAP_Kid14"
/lab_host="DHI0B"
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100.0%; Pred. No. ...
                                                                                                                                                                                                      /note="Vector: pcMV-SPORT6"
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/organism="Mus musculus"
/db_xref="LocusID:72029"
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SOURCE
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Email: cgapbarfemall.nih.gov
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site:
http://www.shgc.stanford.edu
contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
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Location/Qualifiers
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IMAGE:4222133, mRNA, complete cds.
BC013549.1 GI:15488835
MGC.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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Submitted (04-SEP-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        317 cggccggagttgccgttgccgtggttacccagagacacgtgcgcagtcccggaagcgg 376
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                                                                                                                                                                                                                                                                                                                                                                                       79 GGAAAGGACTTTGCCATAGGTCGCTGAGGCCACCATGCTGCTCTTACTGGCCAAGGGCG 138
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8
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                                                                                                                                                                                                                        Score 148.8; DB 9;
Pred. No. 3.3e-24;
0; Mismatches 88;
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/rpt_type=tandem
/rpt_unit=CTG
a 252 c 315 g
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Best Local Similarity 71.3%;
Matches 239; Conservative
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AUTHORS

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/translation="MESMSELAPRCLLEPLLLLPAPKLGFSPAGAEETDWVR
PSKCEVCYVVAVELKSAFEETGKTKEVIDTGYGILDGKGSGVKYTKSDLRILEVTET
ICKRLLDYSLHKERTGSNFRAKGMSETFETLENLVHKGVKYVMDIPYELWNETSBEVA
DLKKQCDVLVPEFEETSYLEDWYRNHQEEDLTPELCANHVLGKGTJSCLAERWGSKKGDI
ASLGGKKSKKKRSGVKGSSSGSSKQRKELGGLGEDANAEEEEGVQKASPLPHSPPDEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs_remail.nh.gov
Tissue Procurement: ATCC
CDNA Library Preparation
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DIN Sequencing by: Institute for Systems Biology
CDNA Sequencing by: Institute for Systems Biology
COORTACT: amadaneSystemsDiology.org
COORTACT: amadaneSystemsDiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Ketteman and Anuradha Madan
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6002306.
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Catarrhini; Hominidae; Homo.
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Submitted (29-MAY-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                           375 ggccgggggaagctgctccgcgcgcgctgccggaggaagcgccggcgggtccgctt434
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/protein_id="AAH08898.1"
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/tissue_type="Colon, adenocarcinoma"
/lab_host="bH10B-R"
/note="Vector: pOTB7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                       20.6%; Score 97; DB 10; I
100.0%; Pred. No. 2.8e-12;
iive 0; Mismatches 0;
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/db_xref="taxon:9606"
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Mammalia; Eutheria; Primates;
1 (bases 1 to 1422)
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97; Conservative
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Best Local (
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DLKKQCDVLVEEFEETJEDWYRNHQEEDLTPETLGANHVLKGKDTSGLAEDWSGKKGDT
AALGGKKSKKKSSRAKAAGGRSSSSKORKELGGLEGDPSPEEDEGIOKASPLTHSPPD
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Homo sapiens, clone MGC:4122 IMAGE:2959532, mRNA, complete cds.
BC008961
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/protein_id="AAH08961:1"
/db_xref="G1:14286320"
/tbanslation="MDSMPEPASRCLLLLPLLLLLLLLLPAPELGPSQAGAEENDWVR
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1422)
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contact: amadan@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Ketteman and Anuradha Madan
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Submitted (29-MAY-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Email: cgapbs-r@mail.nth.gov
Tissue Procurement: ATC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
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/tissue_type="Colon, adenocarcinoma"
/clone_lib="NIH_MGC_15"
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Pred. No. 0.00026;
0; Mismatches 21;
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/db_xref="taxon:9606"
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78.1%;
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HTG 17-MAR-2001
LOW-PASS
           ICKRLLDYSLHKERTGSNRFAKGMSETFETLHNLVHKGVKVVMDIPYELWNEFSAEVA
DLKKOCDVLVEEFEEVTEDWYRNHQEEDLTEFLCANHVLKGKDT SCLAEQWSGKKGDT
AALGGKKSKKKSSRAKAAGGRSSSSKQRKELGGLEGDPSPEEDEGIQKASPLTHSPPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (17-MAR-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA RASearch All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatWasker.html
LPSKCEVCKYVAVELKSAFEETGKTKEVIGTGYGILDQKASGVKYTKSDLRLIEVTET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Center: Whitehead Institute/ MIT Center for Genome Research
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Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
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Pred. No. 0.00026;
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sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low pass sequence sampling is useful for identifying clones that may be gene-rich and allow overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11813: contig of 662 bp in length
14 11913: gap of 100 bp
14 12619: contig of 706 bp in length
20 12719: gap of 100 bp
21 13413: contig of 694 bp in length
14 13513: gap of 100 bp
21 14222: contig of 694 bp in length
21 14222: contig of 709 bp in length
                                                                                                                                                                                                the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 bp
of 703 bp in length
100 bp
of 688 bp in length
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11051: contig of 694 bp in length
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                                NOTE: This record contains 76 individual
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17416: contig of 706 bp
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Center clone name: 430_B_1
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1 (bases 1 to 2028)

Dierlamm, J., Baens, M., Wlodarska, I., Stefanova-Ouzounova, M., Hernandez, J. M., Hossfeld, D.K., De Wolf-Peeters, C., Hagameijar, A., Van den Berghe, H. and Marynen, P.

The apoptosis inhibitor gene APIZ and a novel 18q gene, MLT, are mucosa-associated lymphoid tissue lymphomas

Blood 33 (11), 3601-3609 (1999)
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Dierlamm, J., Baens, M., Wloderska, I., Stefanova-Ouzounova, M., Hernandez, J. M., Hossfeld, D.K., De Wolf-Peeters, C., Hagemeijer, A., Van Den Berghe, H. and Marynen, P.
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Dietlamm,J., Baens,M., Wlodarska,I., Stefanova-Ouzounova,M.,
Hernandez,J.M., Hossfeld,D.K., De Wolf-Peeters,C., Hagemeijer,A.,
Van Den Berghe,H. and Marynen,P.
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On Aug 19, 1999 this sequence version replaced gi:5052334.
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/product="MALT lymphoma associated translocation"
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54065 54164: gap of 100 bp
54165 54875: contig of 711 bp in length
54876 54975: gap of 100 bp
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/map="18q21"
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Seashaghti, Schilbach, S., Koonin, E.V., Aravind, L. and Dixit, V.M.
Direct Submission
Submitted (26-OCT-2000) Molecular Oncology, Genentech Inc., 1 DNA
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1 (bases 1 to 2941)

Koonin, E.V. and Dixit, V.M.

Koonin, E.V. and Dixit, V.M.

Identification of Paracaspases and Metacaspases. Two Ancient Ammilies of Caspase-like Proteins, One of Which Plays a Key Role in the process.
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Submitted (15-JUL-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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                                                            /note="MALT1; MLT1; caspase-like protein"
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                                                                                                                                                           Consensus quality: 169456 bases at least Q40
Consensus quality: 169444 bases at least Q30
Consensus quality: 169444 bases at least Q30
Consensus quality: 205812 bases at least Q30
Consensus quality: 205812 bases at least Q30
Consensus quality: 205812 bases at least Q30
Estimated insert size: 21330; agarose-fp estimation
Quality coverage: 3.43 in Q20 bases; sum-of-contigs estimation
Quality coverage: 3.19 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a working draft' sequence. It currently
* consists of 37 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1422: contig of 1422 bp in length 1522: gap of unknown length 3663: gap of unknown length 4879: contig of 2041 bp in length 4879: contig of 1216 bp in length 6661: contig of 1082 bp in length 6661: contig of 1082 bp in length 7308: contig of 1197 bp in length 8607: contig of 1199 bp in length 8607: contig of 1199 bp in length 8607: contig of 2144 bp in length 10851: contig of 2144 bp in length 10851: contig of unknown length
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contig of 3902 bp in length
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contig of 2915 bp in length
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contig of 3441 bp in length
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Web site: http://www.jgi.doe.gov
                                                                    Center Project Name: 0
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Streptomyces coelicolor A3(2)

Bacteria: Firmicutes; Actinobacteridae;

Actinopacterias: Streptomycineae; Streptomycetaceae; Streptomyces.

(Dases 1 to 36224)

Redenbach, M., Kleser, H.M., Denapaite, D., Eichner, A., Cullum, J.,

Kinashi, H. and Hopwood, D. A.

A set of ordered cosmids and a detailed genetic and physical map

Mol. Microbiol. 21 (1), 77-96 (1996)
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of 6496 bp in length
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of 7888 bp in length
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                                                                                                                                                                                                                                                                                                                         unknown
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                                                                    unknown
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Streptomyces coelicolor cosmid D78.
AL034355

    .230254
    /organism="Mus musculus"
    /db_xref="taxon:10090"
    /clone="RP23-41F9"

   gap of contig contig contig gap of ga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       strand).

The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markow Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/
jun/cgli-bin/framePlot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the most upstream initiation codon. If this cannot be identified we choose the most upstream initiation codon. If this cannot be identified we choose the most upstream initiation codon. If this cannot be identified we choose the most sequenced clone. It may be shorter because we only sequence sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlapping between neighbouring submissions. Cosmid D78 lies to the right of O11 on the Asel-D genomic restriction fragment.

1. 36224

Location/Ouallifiers

1. 36224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="SCD78.01"
/note="SCD78.01, ftsk /spoilib family protein, partial CDS
within putative integrated plasmid, len: 271 aa; similar
to many members of the ftsk /spoilib family e.g.SPI_STRAZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="IGALETGGAWVMNLRLVPHWLIAGATRSGKSTLLARVITQLAPQ
                                                                                                                                                                                                      Submitted (25-NOV-1998) Streptomyces coelicolor sequencing project, Sanitted (25-NOV-1998) Streptomyces coelicolor sequencing project, Sanitted (25-NOV-1998) Streptome Trust Genome Campus, Hinxton, Cambridge (210 ISA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces coelicolor sequencing at The Sanger Centre is funded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              available on the World Wide Web. (URL, http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               by the BBSRC.
Details of S. coelicolor sequencing at the Sanger Centre are
                                                                                                         3 (bases 1 to 36224)
Bentley,S.D., Parkhill,J., Barrell,B.G. and Rajandream,M.A.
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/protein_id="CAA22266.1"
/db_xref="GI:3928710"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:100226"
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                                              Saunders, D.C. and Harris, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /transl_table=11
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to 36224)
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site specific recombinase) from Actinophage R4 (469 aa), fasta scores; opt: 261 z-score: 320.1 E(): 1.4e-10, 29.1% indentity in 306 aa overlap and TR:00604 (EMBL:29586) MTCY356.18 (Rv1886) possible integrase from M tuberculosis integrated phage phiRv1 (469 aa), fasta scores; opt: 371 z-score: 270.8 E(): 7.8e-08, (26.6% identity in 489 aa overlap). Probable colled-coll from 414 to 451 (38 residues) Max score: 1.608 (probability 0.99)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="weethous transpared predefered to the transpared transpared to the transpared transpared to the transpared to the transpared to the transpared transpared to the transpared transpared to the transpared transpared to the transpared transpared transpared to the transpared transpared transpared to the transpared transpared to the transpared t
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wliyyrytdbndksaskesvvrddfeqlladlaagatpegypvhgvmavnddrlyrrps
pwerylkaftsqdgryyhdsnglQdlyaegfeikglvGvamslsetrkkQrrsrnshr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="SCD78.03, possible plasmid replication initiator protein within putetive integrated plasmid, len: 452 aa; protein within putetive integrated plasmid, len: 452 aa; similar to REPS_STRAM (EMBL:219594) replication initiator protein from Streptomyces ambofaciens plasmid pSAM2 (459 aa), fasta scores; opt: 712 z-score: 983.7 E(): 0, (43.7% identity in 467 aa overlap). Note that there is no possible initiation codon upstream of the start of homology (or close downstream). The CDS given here has an arbitrary start.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="hypothetical protein SCD78.02"
/protein_id="CAA22207.1"
/db_xref="GI:3928711"
/translation="MISEGTAFGFAVVFGIITVLLVRSRDVRGWEAVCVGLFGLYLGQ
PVALVGIDCKGGMELGLFADRLSALATSRREAVAVLTALVVDIQERMSACRTAGVRSV
WELPPKLRRYVRVVVLVDEIAELYLSDGTRQSKSEAEQCSTLLLRLAQLGAALGLHLVV
AGORVGSDLGPGVTALRAQLGGRICHRVNDPGTAEMTLGDLNKDAVAVAQAITAQERG
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/transl_table=11
/product="putative plasmid replication initiator protein"
/protein_id="CAA22208.1"
/db_xref="G1:3928712"
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/gene="SCD78.04c"
complement(2805. .4292)
/gene="SCD78.04c. .4292)
/gene="SCD78.04c, possible integrase/ recombinase within putaive integrated plasmid, len: 495 aa; similar to TR:037839 (EMEL:D38173) ORF469 protein (possible gite-specific recombinase) from Actinophage R4 (469 aa),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aa;
                                                                                                                                                                VAVCTGPDGGWARARSHLTPTDEAVATARKHSGMTPELPALDRALVALEGDGK"
                                                                                                                                                                                                                                                                                                                                                                                                                                    /GTP-binding site motif A (P-loop)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="SCD78.02, small hydrophobic protein, len: 65 within putative integrated plasmid"
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/protein_id="CAA22209.1"
/db_xref="G1:3928713"
                                                                                                                                                                                                                                                                               /note="possible integrated element"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TPVLFTIHGLVTWVISGFSHT"
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/gene="SCD78.03"
1308. 2666
                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="PS00017 ATP
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/transl_table=11
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/gene="SCD78.01"
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/gene="SCD78.02"
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/note="SCD78.02,
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/transl_table=11
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                                                                                                                                                                                                                          /gene="SCD78.05"
/fonce="SCD78.05"
/fonce="SCD78.05, thiC', probable thiamin blosynthesis protein thiC, partial CD5, len: 43 aa; simlar to the extreme C-terminus of e.g. THIC_ECOLI thiamin blosynthesis protein thiC (631 aa), fasta scores; opt: 97 z-score: 137.7 E(): 2, 46.2% identity in 39 aa overlap and HIC_MYCTU (547 aa), fasta scores; opt: 143 z-score: 272.4 E(): 6.4e-08, 53.1% identity in 49 aa overlap. Note that this gene appears to have been interrupted by the
KIRERCHGTGTPRGGLVHKYLLTNILBCGNVLEDGTVCNNKMIGIKANDWLKYQHAYM
CKKTVDGGCNKTYKRGDKTDKIIEELVIAKLERDAATKAQDVPDWDKAEALERALQSR
RELERRWHDDEDTDIDDEAFFRNLPVLERRIKELRVDOKAHEALKAEAEBAEABDIRKS
WGAKTLTOKREAMKKVLGAVIALPGGKGNKTFDPDLLKPVWKTSE"
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Submitted (01-APR-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Apr 25, 2001 this sequence version replaced gi:10281392.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 205914)
1 (bases 1 to 205914)
2 Gequencing of Human Chromosome 16
1 (bases 1 to 205914)
2 (bases 1 to 205914)
1 (book Joint Genome Institute.
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/gene="SCD78.06"
/note="SCD78.06, unknown, len: 482 aa; similar
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
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                                                                                                      4444. .4575
/gene="SCD78.05"
/note="thic'"
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4655. .610?
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Consensus quality: 111602 bases at least 040
Consensus quality: 12270 bases at least 030
Consensus quality: 12270 bases at least 030
Consensus quality: 127899 bases at least 020
Estimated insert size: 164311; agarose-fp estimation
Estimated insert size: 164311; agarose-fp estimation
Cuality coverage: 5.85 in 020 bases; agarose-fp estimation
(unality coverage: 4.83 in 020 bases; sum-of-contigs estimation
* NOTE: This is a working draft' sequence. It currently
* consists of 67 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
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                                           Web site: http://www.jgi.doe.gov
Center: Joint Genome Institute
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contig of 1287 bp in length
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contig of 1727 bp in length
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house mouse.

Mus muscullus anschlus anschlus buteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

I (Dasses I to 201324)

Bastide,M., Huang,E.N., King,L., Kirchoff K.N., Miller,B.,

Nascimento,L.U. O'Shaughnessy,A.L., Preston,R.R., Rodriguez,M.A.,

Shah,R.S., Shekher,M., Spiegel,L.A., Toth,K. and Vil,M.D.

Mouse Genomic Sequence

I (Dasses I to 201324)
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Mus musculus clone RP23-185M20, WORKING DRAFT SEQUENCE, 23
unordered pleces.
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Submitted (06-SEP-2000) Lita Annenberg Hazen Genome Sequencing
Submitted (.06-SEP-2000) Lita Annenberg Hazen Genome Sequencing
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ilarity 51.9%; Pred. No. 5;
Conservative 0; Mismatches 91; Indels 0
100318: contig of 2685 bp in length 100418: gap of unknown length 107532: contig of 7114 bp in length 107632: gap of unknown length 119743: contig of 1211 bp in length 119743: contig of 13711 bp in length 13518: contig of 13775 bp in length 13518: contig of 13775 bp in length 13518: contig of 22869 bp in length 156687: contig of 22869 bp in length 156687: gap of unknown length 156687: contig of 49227 bp in length
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/clone_lib="CalTech human BAC library D"
a 42782 c 59428 g 45894 t 13885 others
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Center, Cold Spring Harbor Laboratory,
Harbor, NY 11724, USA
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Web site: http://www.cshl.org/genseq
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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NOTE: This is a 'working draft' sequence. It currently consists of 23 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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39507 c 38629 g 59778 t
                             Center project name: RP23-185M20
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                                          Center clone name: RP23-185M20
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Ouery Match
9.2%; Score 43.2; DB 2; Length 201324;
Best Local Similarity 52.5%; Pred. No. 7.7;
Matches 93; Conservative 0; Mismatches 84; Indels 0;

406 others

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BASE COUNT ORIGIN

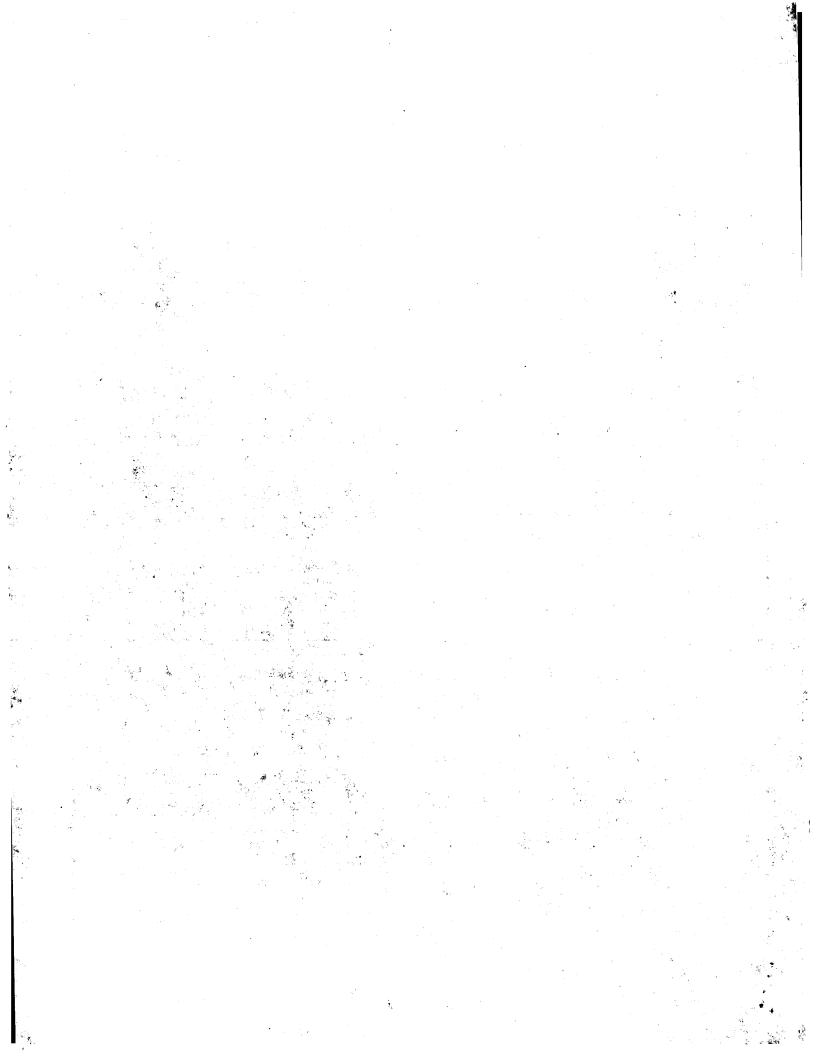
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Search completed: May 24, 2002, 00:18:14 Job time: 11600 sec



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         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Description                   | PCR primer #1 used | Mouse ES cell 7243 | PCR primer #488 us | T243 gene homologo | Murine trinucleori | DNA sequence of an | Human cDNA sequenc | Human EST with Gen | Human cDNA encodin |
|-------------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| SUMMARIES                     | AAS05280           | AAS05287           | AAS05282           | AAS05284           | AAS05278           | AAS05286           | AAS21311           | AAA27030           | AAS26338           |
| DB                            | 22                 | 22                 | 22                 | 22                 | 22                 | 22                 | 22                 | 77                 | 22                 |
| %<br>Query<br>Match Length DB | 25                 | 25                 | 49                 | 471                | 1839               | 1848               | 1675               | 435                | 582                |
|                               | 100.0              | 100.0              | 100.0              | 100.0              | 100.0              | 100.0              | 9.94               | 74.4               | 74.4               |
| Score                         | <br>25             | 25                 | 25                 | 25                 | 25                 | 25                 | 19.2               | 18.6               | 18.6               |
| Result<br>No.                 | 1                  | 0                  | m                  | Ω<br>4             | s<br>S             | 9<br>0             | 0                  | မ                  | 6                  |

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correction (TRR). The invention describes methods of producing embryonic stem (ES) cells comprising a heterozygous disruption in a target DNA sequence (preferably gene T243) encoding a TRP and of producing embryonic sequence (preferably gene T243) encoding a TRP and of producing a knockout mouse comprising a homozygous disruption in a gene encoding TRP, where the disruption inhibits the production of the wild type TRP. The invention also relates to identifying agents capable of affecting a phenotype of a knockout mouse. Also described are methods of determining whether expansion of the trinucleotide repeat in a gene encoding TRP produces a phenotypic change. The transgenic animals and the cells are useful for identifying compounds capable of ameliorating disease symptoms, and as test substrates for the identification of drugs, pharmaceuticals, therapies and interventions which may be effective in transiting trinucleotide repeat disorders e.g. fragile X syndrome and Huntington's disease. The animal models for trinucleotide repeat disorders e.g. traincleotide repeat closel model systems to study the progression of disease in vivo, the molecular basis of these diseases and show the features observed in human disease. Using the mice, it is possible to model both the pathogenic mechanism and the trinucleotide repeat instability in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel transgenic animals useful as animal model for characterization of function of a gene encoding trinucleotide repeat proteins (TRPs), contains heterozygous disruption in a gene encoding TRP -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                 for a trinucleotide repeat
                                                                               for PCR primer #1 is used to amplify sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Trinucleotide repeat protein; TRP; T243; embryonic stem cell; ES; transgenic animal; knockout mouse; triplet repeat expansion;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
contains heterozygous disruption in a gene encoding TRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 25; DB 22; 100.0%; Pred. No. 0.066;
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                                                                                                   homologous to the T243 gene which encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse ES cell T243 gene PCR primer #426.
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                                         Claim 13; Fig 13; 106pp; English
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ID AAS05287 standard; DNA; 25 BP
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Best Local Similarity 100.
Matches 25; Conservative
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Example 12; Fig 13; 106pp; English

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The present sequence for PCR primer #426 is used to amplify the T243

gene from an RI mouse embryonic stem cell genomic library. The T243 gene
encodes for a trinucleotide repeat protein (TRP). The invention describes

ceres for a trinucleotide repeat protein (TRP). The invention describes

ceres for a trinucleotide repeat protein (TRP). The invention describes

ceres encoding TRP, where the disruption inhibits the production on the

configuration in a target DNA sequence (preferably T243) encoding a TRP and

configuration in a target DNA sequence (preferably T243) encoding a TRP and

configuration of the disruption inhibits the production of the

configuration of the invention also relates to identifying agents capable

configuration whether expansion of the trinucleotide repeat in a gene

concoding TRP produces a phenotypic change. The transgenic animals and

the cells are useful for identifying compounds capable of ameliorating

disease symptoms, and as test substrates for the identification of drugs,

configuration trinucleotide repeat disorders e.g. fragile X syndrome and

treating trinucleotide repeat disorders e.g. fragile X syndrome and

the trinucleotide repeat disorders e.g. fragile X syndrome and

confiscents are ideal model systems to study the progression of disease in

convivo, the molecular basis of these diseases and show the features

convivo, the molecular basis of these diseases and show the features

convivors and the trinucleotide repeat instability in the
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Best Local Similarity
Matches 25; Conserv
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from an R1 mouse embryonic stem cell genomic library). Gene T243 encodes for a trinucleotide repeat protein (TRP). The invention describes methods CC of producing embryonic stem (ES) cells comprising a heterozygous disruption in a target DNA sequence (preferably gene T243) encoding a CC in a gene encoding a knockout mouse comprising a homozygous disruption the wild type TRP. Where the disruption inhibits the production of the wild type TRP. The invention also relates to identifying agents CC appable of affecting a phenotype of a knockout mouse. The transgenic animals and the cells are useful for identifying compounds capable of aminals and the cells are useful for identifying compounds capable of aminals and the cells are useful for identifying compounds capable of identification of drugs, pharmaceuticals, therapies and interventions of identification of drugs, pharmaceuticals, therapies and interventions cranged and Huntington's disease. The animal models for trinucleotide repeat disorders are ideal model systems to study the progression of disease in vivo, the molecular basis of these diseases constant instanting the the molecular basis of these diseases of the possible to model both the pathogenic mechanism and the trinucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 49 BP; 8 A; 16 C; 13 G; 12 T; 0 other;
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Gaps
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  Score 25; DB 22; Length 49;
Pred. No. 0.071;
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Trinucleotide repeat protein; TRP: T243; embryonic stem cell; ES;
transgenic animal; knockout mouse; triplet repeat expansion;
fragile X syndrome; Huntington's disease; mouse; ds.
                                                  T243 gene homologous sequence #1 generated by PCR.
AAS05284/c
ID AAS05284 standard; DNA; 471 BP.
                                                                                                                                         26-OCT-2000; 2000WO-US29382.
                                   07-SEP-2001 (first entry)
                                                                                                                                                                                    Klein R, Matthews W,
                                                                                                                                                                      (DELT-) DELTAGEN INC.
                                                                                                           WO200130798-A1.
                                                                                                                                                        26-OCT-1999;
                                                                                                                          03-MAY-2001.
                      AAS05284;
                                                                                              Mus sp.
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Novel transgenic animals useful as animal model for characterization of function of a gene encoding trinucleotide repeat proteins (TRPs), contains heterozygous disruption in a gene encoding TRP Moore M, Allen KD; WPI; 2001-300473/31.

Claim 11; Fig 14; 106pp; English.

PCR The present sequence for T243 homologous sequence #1 is generated by PCR and is homologous to the T243 gene which encodes for a trinuclectide repeat protein (TRP). The invention describes methods of producing embryonic stem (ES) cells comprising a heterozygous disruption in a target DNA sequence (preferably gene T243) encoding a TRP and of producing a knockout mouse comprising a homozygous disruption in a gene

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encoding TRP, where the disruption inhibits the production of the wild affecting a phenotype of a knockout mouse. Also described are methods of determining whether expansion of the trinucleotide repeat in a gene encoding TRP produces a phenotypic change. The transgenic animals and the cells are useful for identifying compounds capable of ameliotating disease symptoms, and as test substrates for the identification of drugs, pharmaceuticals, therapies and interventions which may be effective in treating trinucleotide repeat disorders e.g. fragile X syndrome and the contraction of disorders are ideal model systems to study the progression of disease in ciscoders are ideal model systems to study the progression of disease in cobserved in human disease. Using the mice, it is possible to model both an example.
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                                                                                                                                                                                                                                                                                                  100.0%; Score 25; DB 22; Length 471; 100.0%; Pred. No. 0.092; 1ve 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murine trinucleotide repeat protein (TRP) cDNA sequence.
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ID AAS05278 standard; cDNA; 1839
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Matches 25; Conserv
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(preferably gene T243) encoding a TRP and of producing a knockout mouse comprising a homozygous disruption in a gene encoding TRP, where the disruption inhibits the production of the wild type TRP. The invention of also relates to identifying agents capable of affecting a phenotype of a knockout mouse. Also described are methods of determining whether a knockout mouse. Also described are methods of determining whether can knockout mouse. Also described are methods of determining whether capansion of the transgenic animals and the cells are useful for phenotypic change. The transgenic animals and the cells are useful for identifying compounds capable of ameliorating disease symptoms, and as test substrates for the identification of drugs, pharmaceuticals, therapies and interventions which may be effective in treating to:

Trinucleotide repeat disorders e.g. fragile X syndrome and Huntington's disease. The animal models for trinucleotide repeat disorders are ideal disease. The animal models for trinucleotide repeat disorders are ideal basis of these diseases and show the features observed in human disease. Using the mice, it is possible to model both the pathogenic mechanism and the trinucleotide repeat instability in the mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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/product= "Expanded TRP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ONA sequence of an expanded T243 gene.
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ID AASO5286 standard; DNA; 1848 BP.
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P-PSDB; AAU02500.
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Synthetic.
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The present sequence represents the DNA sequence of an expanded T243

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gene. The T243 gene encodes. for a trinucleotide repeat protein (TRP).

The invention describes methods of producing embryonic stem (ES)

CC cells comprising a heterozygous disruption in a target DNA sequence

CC (preferably gene T243) encoding a TRP and of producing a Knockout mouse

CC comprising a homozygous disruption in a gene encoding TRP, where the

CC comprising a homozygous disruption in a gene encoding TRP, where the

CC also relates to identifying agents capable of affecting a phenotype of

a knockout mouse. Also described are methods of determining whether

C a knockout mouse. Also described are methods of determining whether

C phenotypic change. The transgenic animals and the cells are useful for

cc phenotypic change. The transgenic animals and the cells are useful for

cc phenotypic change. The identification of drugs, pharmaceuticals,

cc therapies and interventions which may be effective in treating

CC therapies and interventions which may be effective in treating

cc trinucleotide repeat disorders e.g. fragile X syndrome and Huntington's

cc disease. The animal models for trinucleotide repeat disorders are ideal

cc model systems to study the progression of disease in vivo, the molecular

model systems to study the progression of disease in vivo, the molecular

cc basis of these diseases and show the features observed in human disease.

CC the trinucleotide repeat instability in the mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cDNA sequence encoding for PRO4409 polypeptide.
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2000WO-US03565
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99WO-US30999
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Best Local Similarity 100.
Matches 25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-FEB-2000;
18-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-FEB-2000;
24-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-FEB-2000;
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30-DEC-1999;
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WPI; 2000-376482/32.
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                                   WO200027865-A1
Homo sapiens.
                                                                                                                                                                                                                                        Borriello F,
                                                                                                                                                           06-NOV-1998;
                                                                                                                   05-NOV-1999;
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Best Local Simi
Matches 21;
                                                                           18-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS21244-AAS21518 encode for novel human secretory and transmembrane
RRO polypeptides. The PRO polypeptides are useful to detect other
RRO polypeptides, to link bloactive molecules to cells expressing
RRO polypeptides, to modulate biological activities of cells expressing
RRO polypeptides, and to detect the presence of mammalian lung, colon,
breast, prostate, rectal, cervical or liver tumours by comparing PRO
polypeptide expression in a cell sample to that in a control sample.
Some of the 275 sequences are also useful to stimulate the release of
tumour necrosis factor alpha (TNF alpha) from human blood, the
proliferation or differentiation of chondrocytes, the proliferation or
gene expression in pericyte cells, the release of proteoglycans from
cartilage, the proliferation of inner car utricular supporting cells or
of T-lymphocytes, the release of a cytchine from peripheral blood
the PRO polypeptides may modulate glucose or free fatty acid uptake by
skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
cof factor VITA. The PRO polypeptides can be used in assays to identify
molecules involved in binding interactions. The polynucleotides encoding
PRO polypeptides can be used to generate probes, antisense RNA/DNA,
transgenic or knock out animals and can be used in gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                    Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bloactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g. lung, breast, prostate, cervical
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                                                                                                                                                                                                                                    Gao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; cbl-SL; proto-oncogene; tyrosine kinase activity modulation;
cancer; carcinoma; cell proliferation; cell differentiation;
cytostatic; gene therapy; EST; expressed sequence tag; ss.
                                                                                                                                                                                                                              Deforge L, Desnoyers L, Filvaroff E, Ga
A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
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87.5%; Pred. No. 39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Fig 135; 813pp; English.
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                                              30-MAR-2000; 2000WO-US08439.
17-MAY-2000; 2000WO-US13705.
22-MAY-2000; 2000WO-US14042.
30-MAY-2000; 2000WO-US14941.
                                                                                                                         02-JUN-2000; 2000WO-US15264.
10-NOV-2000; 2000WO-US30873.
                           2000WO-US07532
                                                                                                                                                                                                                            Beresini M, De
ME, Goddard A,
Stewart TA, Tum
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21; Conservative
                                                                                                                                                                                      (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                       WPI; 2001-408281/43.
                                                                                                                                                                                                                                                                                                                              P-PSDB; AAU12239
                                                                                                                           02-JUN-2000;
                           21-MAR-2000;
                                                                                                                                                                                                                                                 Gerritsen
                                                                                                                                                                                                                              Baker KP,
                                                                                                                                                                                                                                                                 Smith V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Si
Matches 21;
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The present sequence is a numera and recording sequence for the human protein cbl-SL (Y94310), which is believed to play a role in the protein cbl-SL (Y94310), which is believed to play a role in the cregulation of a cell's growth, differentiation and proliferation.

Tregulation of a cell's growth, differentiation and proliferation.

Aberrant expression levels and mutant forms of tyrosine kinases which are the likely targets of cbl-SL have been found in patients with certain types of cancer. The cbl-SL have been found in patients with certain types of cancer. The cbl-SL notleotide sequence was isolated by screening a human pancreatic adenocarcinome cDNA library using the insert of I.M.A.G. E clone ID 526956 from ATCC. Individual cDNA clones were subjected to 3-4 rounds of amplification and purification and several inserts were sequenced. The sequence of the realitication and sequence comparing the cbl-SL DNA or mRNA sequence of the realiting obl-SL full-length comparing the cbl-SL DNA or mRNA sequence in the test sample to the cbl-SL DNA or mRNA sequence in the cost sample to the cbl-SL DNA or mRNA sequence in the cost sample to the cbl-SL DNA or mRNA sequence in the cost sample cot sequence cot show the cbl-SL DNA or mRNA sequence in the cost sample cot sequence cot may also be used in gene therapy and in the construction of a cbl-SL gene concent in cells and animals used to study cbl-SL activity. cbl-SL collypeptides can be used to screen peptide libraries, including partners of the colleging the colleging the colleging the colleging colleging the colleging the colleging the colleging colleging the colleging the colleging colleging the colleging the colleging the colleging colleging the colleging collegin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; immunosuppressive; antiarthritic; ss; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is a human EST with Genbank Accession Number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acids encoding cbl-SL proteins useful for treating cancers expressing a mutant cbl-SL polypeptide .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 therapeutic agent to cancer patients expressing a mutant cbl-SL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74.4%; Score 18.6; C
84.0%; Pred. No. 63;
cive 0; Mismatches
                                                                                                                                                                                              (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 21; Page 71; 77pp; English.
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99WO-US26057
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hyperproliferative disorder; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; cerebral ischaemia; angiogenesis; enervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative. 2000US-0224518. 2000US-0224519. 2000US-0225213. 2000US-0227182 2000US-0227009 2000US-0229287 2000US-0229343 2000US-0225268 2000US-0225758 20000S-0225759 2000US-0226868 2000US-0229345 2000US-0229509 2000US-0229513 2000US-0230438 2000US-0231242 2000US-0231243 20000S-0231244 20000S-0231413 2000US-0215135 2000US-0216647 2000US-0225270 2000US-0226681 2000US-0228924 2000US-0229344 2000US-0230437 2000US-0217496 2000US-0218290 2000US-0220963 2000US-0225214 2000US-0225757 2000US-022526 14-AGG-2000; 18-AGG-2000; 22-AGG-2000; 22-AGG-2000; 32-AGG-2000; 30-AGG-2000; 01-SEP-2000; 01-SEP-2000; 01-SEP-2000; 06-SEP-2000; 06-SEP-2000; 06-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000;

20000S-0240960. 20000S-0241785. 20000S-0241785. 20000S-0241786. 20000S-0241808. 20000S-0241808. 20000S-0241808. 20000S-0241808. 20000S-0246474. 20000S-0246474. 20000S-0246477. 20000S-0246477. 20000S-0234223. 20000S-0234274. 20000S-0234997. 20000S-0235484. 20000S-0235834. 2000US-0236368. 2000US-0236369. 2000US-0236370. 2000US-0236802. 2000US-0237040. 2000US-0239935. 2000US-0239937. 2000US-0249299 2000US-0249300 2000US-0237038 2000US-0237039 2000US-0246528 2000US-0249264 2000US-0236327 2000US-0236367 2000US-0246525 08-NOV-2000) 17-NOV-2000) 17 NOV - 2000; 17 NOV - 2000; 17 NOV - 2000; 17 NOV - 2000; 01 - DEC - 2000; 05 - DEC - 2000; 05 - DEC - 2000; 06 - DEC - 2000; 06 - DEC - 2000; 14-SEP-2000; 21-SEP-2000; 25-SEP-2000; 25-SEP-2000; 26-SEP-2000; 27-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 20-CCT-2000; 20-0CT-2000; 20-0CT-2000; 20-0CT-2000; 01-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 

2000US-0251868 2000US-0251869

08-DEC-2000; 08-DEC-2000; 08-DEC-2000;

2000US-0231968

2000US-0233064

14-SEP-2000;

2000US-0232080 2000US-0232081

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WO200155322-A2
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               The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosain a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunosasays e.g. radioimmunosasays or enzyme linked immunosasays e.g. radioimmunosasays or enzyme linked immunosasays (ELISA). Disorders which are diagnosed or treated immunosorbant assays (ELISA). Disorders which are diagnosed or treated clarificative disorders e.g. rhoumatoid arthritis, hyperproliferative disorders e.g. cardiac arrest, cerebrovascular disorders e.g. oneoplasms of the breast or liver.

Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection, and many other disorders listed in the specification. The polypetides can also be used 'to aid wound healing and epithelial cell proliferation, to prevent skin adian due to subburn. to maintain orans before
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; immunosuppressive; antiarthritic; ss; antirheumatic; cardiant; vasotropic; cerebroprotective; nootropic; cerebroprotective; nootropic; nutbecterial; vituoide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; cerebran disorder; nordensis; nervous system disorder; Alzhelmer's disease; infection; ocular disorder; corneal infection; ocular disorder; skin ageling; epithelial cell proliferation;
                                                                                                                                                                                                                                                New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives .
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84.0%; Pred. No. 65;
live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID No 517; 980pp; English.
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2000US-0251989.
2000US-0251990.
2000US-0254097.
2001US-0259678.
                                                                                                      (HUMA-) HUMAN GENOME SCI INC
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Best Local Similarity 84.0°
Matches 21; Conservative
                                                                                                                                                Rosen CA, Barash SC,
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P-PSDB; AAU16351.
08-DEC-2000; 208-DEC-2000; 211-DEC-2000; 205-JAN-2001; 2
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2000US-0231414.
2000US-0232080.
2000US-0232081.
2000US-0232997.
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2000US-0205515
                        17-JAN-2001; 2001WO-US01341
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17-MAR-2000;
18-APR-2000;
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14-AUG-2000;
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02-AUG-2001
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Ruben SM;

Barash SC,

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2001US-0259678
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08-DEC-2000;
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13-0CT-2000;
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(HUMA-) HUMAN GENOME SCI INC

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The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliozet a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition. Antibodies to the proteins can also. They are also used in alleviating symptoms associated with the disorders and in diagnostic immunoassays eg. radioimmunoassays or enzyme linked immunoassays (ELISA). Disorders which are diagnosed or treated immunosorbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, created autoimmune diseases e.g. rheumatoid arthritis, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. corneal infection, and many other of sorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before can expend this aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to creamate tissues and in chemctaxis. The polypeptides can also be used as food additive or preverview to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present esquence encodes a novel secreted protein of the invention.
                                                                                     New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives - \,
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Pred. No. 68;
                                                                                                                                                                        Claim 1; SEQ ID No 518; 980pp; English.
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AAA27028/c
ID AAA27028 standard; CDNA; 1422 BP.
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84.0%;
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                                WPI; 2001-488783/53:
P-PSDB; AAU16352.
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Best Local Similarity
Matches 21; Conserva
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Rosen CA,
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2000US-0229513.
2000US-0230437.
2000US-0230438.
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2000US-0232080.
2000US-0232081.
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2000US-0214886
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                                                      17-JAN-2001; 2001WO-US01341
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2000US-0229509
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17-MAR-2000;
18-APR-2000;
19-MAY-2000;
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                  02-AUG-2001
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29-SEP-2000;
The present sequence is the largest open reading frame of the human cb. SL. cDNA (AAA27027) which encodes the human protein cbl.SL. cbl.SL. (1s believed to play a role in the regulation of a cell's growth, cf. sepleted to play a role in the regulation of a cell's growth, cf. sepleted to patients with certain types of cancer. The sequence was soldered found in patients with certain types of cancer. The sequence was soldered by screening a human pancreatic adenocarcinoma cDNA ilbrary using the insert of i.M.A.G. E clone iD 526956 from ATCC. Individual cDNA clones were subjected to 3-4 rounds of amplification and purification and several inserts were sequenced. The sequence of the resulting cbl-SL clones were subjected to 3-4 rounds of amplification and purification and several inserts were sequenced. The sequence of a clones were subjected to 3-4 rounds of amplification and purification cc and sequence may be used to screen for the presence of a carcinoma in a subject by comparing the cbl-SL DNA or mRNA sequence in the test sample to the cbl-SL DNA or mRNA of a control sample. Levels of construction of a cbl-SL DNA or mRNA of a control sample. Levels of construction of a cbl-SL pan or mRNA of a control sample. Cc study cbl-SL activity. cbl-SL panel using PRR and Northern blotting. The construction of a cbl-SL gene knockout in cells and animals used to screen peptide binding partners of the cbl-SL protein. These can be used for screening assays, for purification protocols and for interfering construction of a checkly with the functioning of cbl-SL. The protein may also minant chl-sc. Cc be administered as a therapeutic agent to cancer patients expressing a minant chl-sc.
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                                                                                                                                         Novel nucleic acids encoding cbl-SL proteins useful for treating cancers expressing a mutant cbl-SL polypeptide .
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Best Local Similarity 84.0%; Pred. No. 71;
Matches 21; Conservative 0; Mismatches
        (BGHM ) BRIGHAM & WOMENS HOSPITAL INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Page 70-71; 77pp; English.
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                                              Borriello F, Band H;
                                                                                WPI; 2000-376482/32.
P-PSDB; AAY94330.
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AAS25883/C
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à g New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives -

WPI; 2001-488783/53.

P-PSDB; AAU15896

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(HUMA-) HUMAN GENOME SCI INC
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2000US-0237038
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2000US-0246476
                                                                                                                              2000US-0237039
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05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 20-SEP-2000; 20-SE
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17-NOV-2000;
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The invention relates to isolated nucleic acid molecules and their cocced secreted proteins. The nucleic acids and proteins are used to provent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They muse, mice, crabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays (ELISA). Disorders which are diagnosed or treated immunosorbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis.

Conclude autoimmune diseases e.g. rependance of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. corneal infection, and many other of disorders e.g. corneal infection, and many other consisted in the specification. The polypetides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to subburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to creame a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, cofactors and other nutritional components. The present escape or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, cogequence encodes a novel secreted protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74.4%; Score 18.6; E
84.0%; Pred. No. 72;
Live 0; Mismatches
                                                                                                                               Claim 1; SEQ ID No 62; 980pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human polynucleotide SEQ ID NO 164.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAK51619 standard; cDNA; 1526 BP
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2000US-0654936.
2000US-0663561.
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Matches 21; Conserv
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01-SEP-2000;
15-SEP-2000;
20-OCT-2000;
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20-JUN-2000;
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2000US-0693325

Ruben SM;

Barash SC,

Rosen CA,

Ma Y;

Cao Y,

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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hemmatopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing
                                                                                                                                                                                                                                     Nucleic acids encoding polypeptides with cytokine-like activities,
                                                                                    Drmanac RT, Asundl V, Zhou P, Xu C, Cao Y Wang J, Zhang J, Ren F, Chen R, Wang ZW; Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; proto-oncogene; tyrosine kinase activity modulation; cancer; carcinoma; cell proliferation; cell differentiation; cytostatic; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1543 BP; 306 A; 515 C; 470 G; 252 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22;
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84.0%; Pred. No. 72;
iive 0; Mismatches
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                                                                                                                                                                                                                                                          useful in diagnosis and gene therapy
                                                                                                                                                                                                                                                                                                 Claim 1; Page 4504; 6221pp; English.
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13..1437
/*tag= a
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    30-NOV-2000; 2000US-0728422
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                                                                                                                                                                    WPI; 2001-476283/51.
P-PSDB; AAM79470.
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                                                                                  Liu C, D
Wang D,
Yang Y, W
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                                             (HYSE-) HYSEQ INC
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                                                                                    Tang YT,
Zhao QA,
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                                                                                                                                                                                                                                                                                                                                                   encoded polypeptides (AAM78323-AAM880302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymeredides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; cytokine; cell proliferation; cell differentiation; gene therapy; accine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
                                                                                      Ma Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: Records for SEQ ID NO 2110 (AAK$2581), 2111 (AAK$2582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                    The invention relates to polynucleotides (AAK51456-AAK53435) and the
                                                                                                                                                                                                                              Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy
                                                                                Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW; Yang Y, Wejhrman T, Goodrich R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1526 BP; 303 A; 505 C; 465 G; 253 T; 0 other;
                                                                                                                                                                                                                                                                                           Claim 1; Page 889-891; 6221pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human polynucleotide SEQ ID NO 2132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAK52603 standard; cDNA; 1543 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; 2000US-0496914.
; 2000US-0560875.
; 2000US-0598075.
; 2000US-0620325.
; 2000US-0654936.
; 2000US-0663561.
30-NOV-2000; 2000US-0728422
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Best Local Similarity 84.0°
Matches 21; Conservative
                                                                                                                                                                  WPI; 2001-476283/51.
                                           (HYSE-) HYSEQ INC
                                                                                                                                                                                       P-PSDB; AAM78486
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20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
15-SEP-2000;
20-OCT-2000;
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                                                                                Tang YT,
Zhao QA,
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Indels

Length 1543;

Band H; Borriello F,

WPI; 2000-376482/32.

P-PSDB; AAY94330

Novel nucleic acids encoding cbl-SL proteins useful for treating cancers expressing a mutant cbl-SL polypeptide

Claim 2; Page 67-69; 77pp; English.

The present sequence encodes the numan process to a cell's growth, differentiation and proliferation. Aberrant expression levels and mutant offerms of tyrostime kinases which are the likely targets of cols. Lave been found in patients with certain types of cancer. The sequence was been found in patients with certain types of cancer. The sequence was solated by screening a human pancreatic adenocarcinoma cDNA library using the inserts of I.M.A.G. E clone ID 526956 from ATCC. Individual CDNA clones were subjected to 3-4 rounds of amplification and purification and several inserts were sequenced. The sequence of the resulting cbl-SL cull-length clone was confirmed on more independent clones. The nucleic acid sequence may be used to screen for the presence of a carcinoma in a subject by comparing the cbl-SL DNA or mRNA sequence in the test sample to the cbl-SL DNA or mRNA of a control sample. Levels of cbl-I expression may be measured using prof and nother blotting. The construction of a cbl-SL general in cells and animals used to study cbl-SL activity. cbl-SL polypeptides can be used to screen peptide libraries, including phage display libraries, to identify and select or screening assays, for purification protein may also coll-SL protein. These can be used for interfering directly with the functioning of cbl-SL. The protein may also be administered as a therapeutic agent to cancer patients expressing a The present sequence encodes the human protein cbl-SL, which is 

Sequence 1547 BP; 313 A; 513 C; 468 G; 253 T; 0 other;

Gaps ; 0 Query Match
74.4%; Score 18.6; DB 21; Length 1547;
Best Local Similarity 84.0%; Pred. No. 72;
Matches 21; Conservative 0; Mismatches 4; Indels 0;

; 0

1 agctcagacatggactccatggccc 25 ò

1061 AGCTCAAATGTGGAGTCCATGGCCC 1037 q

Search completed: May 24, 2002, 00:23:09 Job time: 9006 sec

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Search completed: May 24, 2002, 00:18:05
Job time: 11551 sec
                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
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Sequence 9, Application US/09442629
Sequence 10. 6291219
GENERAL INFORMATION:
APPLICANT: TATURUCHI, Naoyuki
SHIBA, TATESON
TITLE OF INVENTION: Alpha 1-6 Fucosyltransferase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Kenyon & Kenyon
STRET: 1025 Connecticut Avenue, N.W., Suite 600
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3;
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MEDIUM TYPE: 3+ FLOPPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: Wordberfect 6.1 Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/442,629
FILING DATE: 18-NO. 6291219-1999
PRIOR APPLICATION NUMBER: PCT/JP97/00171
FILING DATE: 7 JAN 1997
APPLICATION NUMBER: PCT/JP97/00171
FILING DATE: 23 JAN 1997
APPLICATION NUMBER: JP 192260
FILING DATE: 22 JUL 1996
APPLICATION NUMBER: JP 192260
FILING DATE: 22 JUL 1996
APPLICATION NUMBER: JP 162813
FILING DATE: 24 JUN 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 16.4; DE Pred. No. 86; 0; Mismatches
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JD97/00171
FILING DATE: 23 JAN 1997
APPLICATION NUMBER: JP 16280
FILING DATE: 22 JUL 1996
APPLICATION NUMBER: JP 162813
FILING DATE: 24 JAN 1996
APPLICATION NUMBER: JP 161648
FILING DATE: 21 JUN 1996
APPLICATION NUMBER: JP 10365
FILING DATE: 21 JUN 1996
APPLICATION NUMBER: JP 10365
FILING DATE: 24 JAN 1996
APPLICATION NUMBER: JP 10365
FILING DATE: 24 JAN 1996
APPLICATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 39,048
TELEPHONE: 202-429-1776
TELEPAX: 202-429-1776
TELEPAX: 202-429-1776
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
LENGTH: 2100 base pairs
TYPE: NUCLEIC GAID
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 94.4'
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA US-08-913-805A-9
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Gaps
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APPLICATION NUMBER: JP 161648
FILING DATE: 21 JUN 1996
APPLICATION NUMBER: JP 10365
FILING DATE: 24 JAN 1996
ATTORNEY AGENT INFORMATION:
REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 2356/3
TELECHONUNICATION INFORMATION:
TELEPRAX: 202-429-0796
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2100 Dase Pairs
                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: Innear
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-442-629-9
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE REPERENCE: P99-2-6
FILE REFERENCE: P99-2-6
CURRENT APPLICATION NUMBER: US/09/239,909
CURRENT APPLICATION NUMBER: EP 99300136.1
EARLIER APPLICATION NUMBER: EP 99300136.1
NUMBER OF SEQ ID NOS: 4
SOFTWARE: KOPATIN 1.0
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                                                                                                                                                Gaps
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                                                                                                     67.2%; Score 16.8; DB 2; Length 4534; 90.0%; Pred. No. 63; tive 0; Mismatches 2; Indels 0
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Sequence 9, Application US/08913805A
Patent No. 6054304
GENERAL INFORMATION:
APPLICANT: TANIGUCHI, Naoyuki
APPLICANT: TANIGUCHI, Naofumi
APPLICANT: SHIBA, Tetsuo
APPLICANT: SHIBA, Tetsuo
APPLICANT: SHIBA, Tetsuo
APPLICANT: ANAGIDANI, Shusaku
TITLE OF INVENTION: Alpha 1-6 Fucosyltransferase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W., Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 16.6; DB; Pred. No. 62; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: 3+ Floppy disk COMPUTER: 1BM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS 6.2 SOFTWARE: WordPerfect 6.1 Windows CURREWT APPLICATION DATA: APPLICATION NUMBER: US/08/913,805A FILLING DATE: 7 JAN 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: G. max calmodulin5 (SCaM5)
                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09239909
Patent No. 6284952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 agctcagacatggactccatggc 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 agctcaaacattaacaccatggc 73
                                                                                                                                                                                                                  2686 CAGAGATGGTCTCCATGGCC 2667
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82.6%;
                                                                                                                                                                                        5 cagacatggactccatggcc 24
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Best Local Similarity 82.6
Matches 19; Conservative
                                                                                                             Query Match
Best Local Similarity 90.03
Matches 18; Conservative
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MEDIUM TYPE: 3+ Flop
          ; NAME/KEY: CDS
; LOCATION: (757)...(3771)
US-08-935-450-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: CDS
; LOCATION: (69)..(518)
US-09-239-909-3
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STATE: D
COUNTRY:
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US-09-239-909-3
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0
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE AND USES THEREFOR.
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS: LENERS, DAYLD, LITTENBERG, KRUMHOLZ & MENTLIK
STREET: GOO SOUTH, AVENUE WEST
CITY: WESTFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCHERING 3.0-017 CIP CIP IV
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Sequence 1, Application US/08935450
Patent No. 5977311
GENERAL INFORMATION:
APPLICANT: Nandabalan, Krishnan
APPLICANT: Yang, Meijia
TITLE OF INVENTION: 53BPZ COMPLEXES
FILE REFERENCE: 7934-054
CURRENT FILIGATION NUMBER: US/08/935,450
CURRENT FILIGATION NUMBER: US/08/935,450
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67.2%; Score 16.8; 90.0%; Pred. No. 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: misc_feature
; LOCATION: 1..2205
; OTHER INFORMATION: /note= "mutTM1-TM2"
US-08-888-077A-41
                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 07090-1497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/88,077A
FILING DATE: 03-JUL-1997
CLASSIFCATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/59,541
FILING DATE: 20-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: PALISI, THOMAS M
REGISTRATION NUMBER: 36,629
REFERENCE/DOCKET NUMBER: SCHERING 3.-
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2205 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TOPPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DD 1055 AACTCAGACATGGACTACAT 1074
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Best Local Similarity 90.0
Matches 18; Conservative
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SEQUENCE CHARACTERISTICS

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356 AACTCAGACATGGACTACAT 375
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OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 2036 base pairs
TYPE: nucleic acid
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Best Local Similarity 90.0
Matches 18; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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ORIGINAL SOURCE:
ORIGINAL SOURCE:
US-08-923-454A-17
                                                                                                                                                                                                                                                                                                                                                                                          USA
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                                                                                                                                                                                                                                                                                                                                                          US-08-322-742-18
Sequence 18, Application US/08322742
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
SARREFT: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUD TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION NUMBER: US/08/322,742
                                                                                                                                                                                              ch 68.0%; Score 17; DB 1. Similarity 80.0%; Pred. No. 60; 20; Conservative 0; Mismatches
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90.0%; Pred. No. 47;
tive 0; Mismatches
LENGTH: 15079 base pairs
TYPE: nucleic acid
STANDEDNES: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               00530/048003
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APPLICATION NUMBER: 07/938,823
FILING DATE: September 1, 1992
APPLICATION NUMBER: 07/844,296
FILING DATE: February 28, 1992
APPLICATION NUMBER: 07/552,216
FILING DATE: February 28, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
                                                                                                                                                                                                                                                                                       Db 3623 AGCTCCGACCTGGAGACCATCGCCC 3647
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REFERENCE/DOCKET NUMBER: 0053(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELERAX: (617) 542-8906
TELEX: 200154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 90.0%
Matches 18; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 20; Conserva
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STREET: 440
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US-08-322-742-18
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90.0%; Pred. No. 56;
tive 0; Mismatches 2;
                              APPLICANT: Creasy, Caretha
APPLICANT: Liv1, George
APPLICANT: Liv1, George
APPLICANT: Clinkenbeard, Helen
APPLICANT: Clinkenbeard, Helen
APPLICANT: Southan, Christopher
TITLE OF INVENTION: HUMAN SERINE PROTEASE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Smith***
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Feature polymorphism at 1325
                                                                                                                                                                                                                                                SSEE: SmithKline Beecham Corporation
F: 709 Swedeland Road
King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FEASTER DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,454A
US-08-923-454A-17; Sequence 17, Application US/08923454A; Sequence 10. 6004794; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
US-08-888-077A-41
Sequence 41, Application US/08888077A
Patent No. 6020143
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P50547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/025436
FILING DATE: 06-SEPT-1996
ATTORNEY/AGENT INFORMATION:
NAME: BAUMBISELE, KITK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33,833
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Susan E. Jensen
APPLICANT: Kwamena A Aidoo
APPLICANT: Ashish S. Paradkar
TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic
Patent No. 6232106
TITLE OF INVENTION: Acid Biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                68.0%; Score 17; DB 4; Length 11604;
80.0%; Pred. No. 58;
Live 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUDRESSEE: JACOBSON, PRICE, HOLMAN & STERN, PPLC STREET: The Jenifer Bullding, 400 Seventh Street, N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/385,028
                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/790,462
PILLING DATE: 29-JAN-1997
ATTORNEY/AGENT INCOMANTION:
NAME: D. DOUGLAS PRICE
REFERENCE/DOCKET WUMBER: 1418/P57452US2
TELECOMUNICATION INFORMATION:
TELEPRAN: (202 638-6666
TELEPRAN: (202) 39305350
TELEPRAN: (202) 39305350
TELEPRAN: (202) 39305350
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/790,462
FILING DATE: 29-JAM-1997
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US/09/385,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1591 AGCTCCGACCTGGAGACCATCGCCC 1615
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REFERENCE/DOCKET NUMBER: 1418
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202 638-666
TELEFAX: (202) 39305350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09385028 Patent No. 6232106
                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: DNA (genomic) US-09-385-028-13
                                                                                                                                                                                                                                                                                LENGTH: 11604 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: D. Douglas Price
REGISTRATION NUMBER: 24
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 68.0°
Best Local Similarity 80.0°
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 2:
CORRESPONDENCE ADDRESS:
ADDRESSEE: JACOBSON,
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                                                                                                                                                                                                                                                                                                                                         linear
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              APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
APPLICANT: Spaulding, Vikki
APPLICANT: Spaulding, Michael J.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN, PPLC STREET: The Jenifer Buliding, 400 Seventh Street, N.W. CIIY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 80.0%; Pred. No. 48;
Matches 20; Conservative 0; Mismatches
                                                                                                                                                     ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 1977 AGCAGAGACAAGGAGGCCATGGCCC 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ageteagaeatggaeteeatggeee 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                            02140
P PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U.S.A.
                                                                                                                                                                                            Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U. ZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-014-969-10
                                                                                                                                                                                          CITY: Cal
STATE: M.
COUNTRY:
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATORNEY/AGENT INFORMATION:
NAME: D. DOUGJAB PRIOC
RECISTRATION NUMBER: 24,514
RECISTRATION NUMBER: 1418/P57452US2
TELECOMMUNICATION INCHARTION:
                                   Db 1408 AGCTCCGACCTGGAGACCATCGCCC 1432
                                                                                                             RESULT 5
US-09-385-028-15
Sequence 15, Application US/09385028
Patent No. 6232106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 agctcagacatggactccatggccc 25
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Patent No. 5965397
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (202 638-6666
TELEFAX: (202) 39305350
TELEFAX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1722 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ·MOLECULE TYPE: DNA (genomic) US-09-385-028-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 80.0 Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-440A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: WINTER, Claire M.
APPLICANT: WINTER, John C.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2.
SOFTHARE: PATENTIN VEr. 2.1
                                                  Gaps
                                                                                                                                                                                                                                                        GENERAL INFORMATION:

APPLICANT: FLEISCHMAN, Robert D.

APPLICANT: HITE, Owen R.

APPLICANT: WITE, Owen R.

APPLICANT: VENTER, John C.

TITLE OF INVENTION: TUBERCULOSIS

FILE REPERENCE: 24366-20007.00

CURRENT APPLICATION NUMBER: US/09/103,840A

CURRENT FILING DATE: 1998-06-24

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PATENTI VET. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 4411529;
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        DB 4; Length 7720;
                                              4; Indels
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Query Match 70.4%; Score 17.6; E Best Local Similarity 83.3%; Pred. No. 29; Matches 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 68.8%; Score 17.2; D
Best Local Similarity 86.4%; Pred. No. 47;
Matches 19; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68.8%; Score 17.2; D
86.4%; Pred. No. 47;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA .ORGANISM: Mycobacterium tuberculosis
                                                                             ; TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
                                                                                                                                                                                                                      Sequence 2, Application US/09103840A
Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 gctcagacatggactccatggc 23
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Best Local Similarity 86.4
Matches 19; Conservative
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                                                                                                                                                                                RESULT 3
US-09-103-840A-2/c
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US-09-103-840A-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 2
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GENERAL INFORMATION:
APPLICANT: Susan E. Jensen
APPLICANT: Susan E. Jensen
APPLICANT: Susan E. Jensen
APPLICANT: Ashlash S. Paradkar
TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic
Patent No. 6232106
TITLE OF INVENTION: Acid Biosynthesis
CORRESPONDENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN, PPLC
STREET: The Jenifer Buliding, 400 Seventh Street, N.W.
CITTY: Washington.
STRATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68.0%; Score 17; DB 4; Length 1722;
80.0%; Pred. No. 45;
1.ve 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/385,028
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Jacobs, Kenneth
APPLICANT: MCCOy, John M.
APPLICANT: LaVallie, Edward R.
APPLICANT: Racie, Lisa A.
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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 23, 2002, 21:05:34; Search time 121:39 Seconds

(without alignments)
50.588 Million cell updates/sec

Perfect score: 25
Sequence: 1 agctcagacatggactccatggccc 25
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Total number of hits satisfying chosen parameters: 767066

383533 segs, 122816752 residues

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0

Scoring table:

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*

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6: \cgn2\_6/\ptodata/1/\ina/PCTUS\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Description         |                  | Sequence 5, Appli | n.        | i,      | 12               | 10         | Sequence 13, Appl | -         |        | Sequence 17, Appl | _                 | H,   | Sequence 3, Appli | Sequence 9, Appli | o,              | ì               | Ţ,               | Sequence 1, Appli | Sequence 1, Appli | Sequence 1, Appli | H               |           | Sequence 8, Appli | 14,  | ٠,              | Sequence 1, Appli | Sequence 2, Appli |
|---------------------|------------------|-------------------|-----------|---------|------------------|------------|-------------------|-----------|--------|-------------------|-------------------|------|-------------------|-------------------|-----------------|-----------------|------------------|-------------------|-------------------|-------------------|-----------------|-----------|-------------------|------|-----------------|-------------------|-------------------|
| D                   | US-09-318-448-20 | US-09-318-448-5   | -103-840A | 3-840A  | US-09-385-028-15 | -014-969-1 | -09-385-028       | -09 - 385 | -08-32 |                   | US-08-888-077A-41 |      | US-09-239-909-3   | US-08-913-805A-9  | US-09-442-629-9 | US-08-890-853-1 | US-09-099-125A-1 | US-09-099-124A-1  | US-09-197-008-1   | US-09-032-476-1   | US-08-890-854-1 | -023-324- | -08-910-          | 8    | US-09-215-131-1 | -222-734          | US-08-751-189-2   |
| B0                  | 4                | 4                 | 4         | 7       | 4                | 7          | 4                 | 4         | -      | 3                 | ٣                 | 7    | 4                 | ٣                 | 4               | ~               | 7                | 7                 | ~                 | 4                 | 4               | 4         | 4                 | 4    | ٣               | m                 | 7                 |
| gth                 | 3228             | 7720              | 4403765   | 4411529 | 1722             | 2925       | 11604             | 15079     | 539    | 2036              | 2205              | 4534 | 916               | 2100              | 2100            | 2268            | 2268             | 2268              | 2268              | 2268              | 2268            | 2268      | 2271              | 2931 | 3966            | 3966              | 7886              |
| %<br>Query<br>Match | 70.4             | 70.4              | æ         | 68.8    | 68.0             | 68.0       | 68.0              |           | 67.2   |                   |                   | 67.2 |                   | 9.59              | 9.59            |                 |                  | 64.8              |                   | 64.8              | 64.8            | 64.8      | 64.8              | 64.8 | 64.8            | 64.8              | 64.8              |
| Score               | 17.6             | 17.6              | 17.2      | 17.2    | 17               | 17         | 17                | 17        | 16.8   | 16.8              | 16.8              | 16.8 | 16.6              | 16.4              |                 | 16.2            |                  |                   | •                 |                   |                 |           |                   |      |                 | 16.2              | •                 |
| Result<br>No.       | 1                | 7                 | о<br>О    | C 4     | 5                | 9          | 7                 | 8         | 6      | 10                | 11                | c 12 |                   | c 14              | c 15            | -               | -                | c 18              | ٦                 | ~                 | c 21            | 7         | C                 | N    | CA              | c 26              | c 27              |

| Sequence 2, Appli | Sequence 2, Appli | Sequence 5, Appli | Sequence 15, Appl | Sequence 1, Appli | Sequence 7, Appli | Sequence 3, Appli | Sequence 3, Appli | Sequence 1, Appli | Sequence 1, Appli | Sequence 1, Appli | Sequence 1, Appli | Sequence 46, Appl | Sequence 48, Appl | Sequence 47, Appl | Seguence 246, App  | Sequence 20, Appl | Sequence 7, Appli |  |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|-------------------|-------------------|--|
| US-09-060-836-2   | US-09-184-445-2   | US-08-836-075A-5  | US-08-651-136C-15 | US-09-019-689-1   | US-08-253-155A-7  | US-08-449-644-3   | US-08-087-244A-3  | US-08-068-945A-1  | US-08-442-806-1   | US-08-758-621-1   | US-09-107-858-1   | US-09-268-992-46  | US-09-268-992-48  | US-09-268-992-47  | US-08-936-165A-246 | US-09-541-941B-20 | US-08-545-809A-7  |  |
| 7                 | 4                 | 4                 | m                 | e                 | Н                 | 7                 | ~                 | Н                 | Н                 | 7                 | 4                 | 4                 | 4                 | 4                 | 4                  | 4                 | 'n                |  |
| 7886              | 7886              | 327               | 808               | 2415              | 3407              | 4374              | 4374              | 11531             | 11531             | 1329              | 1329              | 2464              | 2488              | 3016              | 3323               | 815               | 877               |  |
| 64.8              | 64.8              | 64.0              | 64.0              | 64.0              | 64.0              | 64.0              | 64.0              | 64.0              | 64.0              | 63.2              | 63.2              | 63.2              | 63.2              | 63.2              | 63.2               | 62.4              | 62.4              |  |
| 16.2              | 16.2              | 16                | 16                | 16                | 16                | 16                | 16                | 16                | 16                | 15.8              | 15.8              | 15.8              | 15.8              | 15.8              | 15.8               | 15.6              | 15.6              |  |
| 28                | 59                | 30                | 31                | 32                | 33                | 34                | 35                | 36                | 37                | 38                | 39                | 40                | 41                | 42                | 43                 | 44                | 45                |  |
| υ                 | U                 |                   |                   | Ų                 | U                 |                   |                   |                   |                   |                   |                   |                   |                   |                   | U                  | ,                 |                   |  |
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## ALIGNMENTS

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High quality sequence stop: 262.

Location/Qualifiers
1.651

Location/Qualifiers
1.651

/organism="Mus musculus"
/strain="C57/B6"
/db-xref="Laxon:10090"
/clone="IMAGE:3484616"
/clone="IMAGE:3484616"
/clone="IMAGE:3484616"
/clone="ID="NCI_CGAP_Mam5"
/tab.host="T months"
/lab.host="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not!; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH."
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                                                                                                                                                                                                                                                                                    163
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ORIGIN
                    FEATURES
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Search completed: May 23, 2002, 23:05:27 Job time: 7483 sec

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TITLE
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BE289316/c
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
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RIKEN Wouse ESTS (Arakawa, T., et al. 2001)

AL Unpublished (2001)

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (SC), Yokohama Institute

Sciences Center (SC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)

1.7-22 Suehiro-Cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000) Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: genome_resegsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Carninci,P., Shibata,Y., Hayatsu,N., and Hayashizak,Y.
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
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BB652011
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0; Mismatches
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Fax: 81-45-503-9216
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Matches 25; Conservative
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KEYWORDS
SOURCE
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à g COMMENT

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/organism="was misserials
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/clone="misserials"
/clone="id="RKEN [uil-length enriched, ES cells"
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Computer-based methods for the mouse full-length CDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Yamanaka,I., Kiyosawa,H., Kondo,S., Saito,P., Shinagawa,A., Aizawa,Y., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shinata,K., Arakawa,T., Ishii,Y. and Hayashizaki,Y. Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct. Func. Genomics 2 pre, L72-L86 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
Tissue Procurement: Lothar Humphreys
Tissue Procurement: Lothar Humphreys
Tissue Procurement: Lothar Humphreys
Tissue Procurement: Lothar Humphreys
Tissue Ph.D., Robin Humphreys
Tissue Procurement: Lothar Humphreys
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1. 649
/organism="Mus musculus"
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(10), 1757-1771 (2000)

(11), 1757-1771 (2000)

(11), 1757-1771 (2000)

(12), 281-187 (2001)

(13), 281-289 (2001)

(14), 281-289 (2001)

(15), Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,H., Aixawa,H., Yamanaka,I., Aizawa,H., Aixawa,H., Aix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: genome resigns.riken.go.jp,
URL:http://genome.go.gr.criken.go.jp,
Carninci.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Carninci.p., Shibata,Y., Hayatsu,N., and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi.K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y.
                                                                                                                                                                                                Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Caboratory for Genome Exploration Research Group, RIKEN Genomic
Catences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTS (Arakawa,T., et al. 2001)
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/db_xref="taxon:10090"
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/clone_lib="RIKEN full-length enriched, adult male aorta
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Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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/dev_stage="adult"
/lab_host="DH108"
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                                                                                                                                                               Unpublished (2001)
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Score 25; DB 9; Length 641; Pred. No. 4;

100.0%;

Query Match Best Local Similarity

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Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria: Rodentia; Sciurognathi; Muridae; Murinae; Mus. (Bassa; 1co 64).

Eukaryota: Metazoa: Chordata; Sciurognathi; Muridae; Murinae; Mus. (Bassa; 1co 64).

M. Hiramoto, K., Horli, F., Ishil, Y., Ito, M., Rawai, J., Ronno, H., Kouda (Mazaki, Y., Okida, K., Batto, R., Sakai, C., Sakai, K., Sano, H., Kouda (Mazaki, Y., Okida, K., Salto, R., Sakai, C., Sakai, K., Sano, H., Sasaki, J., Shipata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takabashi, F., Takeda, Y., Tanaka, T., Toya, T., Riken Mouse ESTS (Arakawa, T., et al. 2001)

Rontamatsu, M. and Hayashizaki, Y.

Riken Mouse ESTS (Arakawa, T., et al. 2001)

Contact: Yoshihide Hayashizaki, T.

Riken Mouse ESTS (Arokawa, T., et al. 2001)

Contact: Yoshihide Hayashizaki, T.

Riken Mouse ESTS (Arokawa, T., et al. 2001)

Contact: Yoshihide Hayashizaki, T.

Riken Mouse ESTS (Arokawa, T., et al. 2001)

Contact: Yoshihide Hayashizaki, Y.

Riken Mouse ESTS (Arokawa, T., et al. 2001)

Contact: Yoshihide Hayashizaki, Y.

Riken Hayashizaki, Y.

Ronno, H., Okazaki, Y. Hayatsu, M., Sugahara, Y., Shibata, K., Itoh (M., Shibata, Y., Hayashizaki, Y., Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length CDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

Waqi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watali, Y., Warahiki, M., Yoneno, H., Waranishiki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN Integrated Sequence analysis (RISA) system--184-format Sequencing pipeline With 34 multicapillary sequencer. Genome Res. 10 (11), 117-177171 (2000)

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Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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BB661603.1 GI:16495382
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/lab_host="DH10B"
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25; Conservative
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Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,R., Hori,F., Ishii,Y. Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki, D., Shibata,K., Shinagawa,A., Shiraki,T., Saito,R., Sano,H., Sasaki, D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabo,Y., Suzuki,H., Tagami,M., Tagawa,A., Takakaki,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.

RIKEN Mouse ESTS (Arakawa,T., et al. 2001)

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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh

Carninci, P., Shibata, Y., Hayatsu, N., and Hayashizaki, Y.

M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNs to

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genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,

Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura

Hayashizaki, Y.
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BB650071 GI:16484326
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/tissue_type="spinal cord"
/dev_stage="adult"
/lab_host="DH10B"
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Best Local Similarity 100.
Matches 25; Conservative
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AUTHORS
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LOCUS

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 641)
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A. Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Saaki,Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
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                                                                                                                                                                                 Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/db_xref="taxon10090"
/clone="c23003960s"
/clone_lib="RIKEN full-length enriched, 0 day neonate
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/dev_stage="0 day neonate"
/lab_host="DH10B"
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Gaps

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REFERENCE AUTHORS

TITLE JOURNAL COMMENT

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Contact: Yoshhide Hayashizaki
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Tel: 81-45-503-9212
Fax: 81-45-503-9216
Fax: 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Atakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Horli, F., Ishil, Y., Ito, M., Kawai, J., Konno, H., Kouda Okazaki, Y., Okido, T., Miyazaki, A., Nomura, K., Ohno, M., Shibata, K., Shinagawa, A., Shiraki, Y., Sogabe, Y., Sauo, H., Sasaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, M., Tagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Muramatsu, M., Tagawa, A., Takabashi, F., Takeda, Y., Tanaka, T., Toya, T., RIKEN, Mouse, ESTS, (Arakawa, T., et al. 2001)
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Computer-based methods for the mouse full-length cDNA
Computer-based methods for the mouse full-length cDNA
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Kondo,S., Shinagawa,A., Salto,T., Kiyosawa,H., Yamanaka,I., Aizawa
.K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
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Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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BB633565.1 GI:16469889
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Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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               DB 9;
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               Score 25;
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URL: http://genome-reségac.riken.go.jp,
URL: http://genome-gac.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
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Computer-based methods for the mouse full-length cDNA
encyclopedla: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Salto,T., Kiyosawa,H., Yamanaka,I., Aizawa
Hayashizaki,Y.
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/lab_host="DHIOB"
/lab_host="Dhiostopedia"
/lab_host="Dhiostope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-25 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
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Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="D630017H14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Yoshihide Hayashizaki
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source

FEATURES

/sex="male"

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BASE COUNT ORIGIN

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AL Unpublished (2001)
On Dec 5, 2000 this sequence version replaced gi:11557214.
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
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URL:http://genome.gsc.riken.go.jp/
URL:http://genome.gsc.riken.go.jp/
Caraninci,P., Shibata,Y., Hayatsu,M. and Hayashizaki,Y. Itoh
'M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapped discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
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/clone="INGE:422133"
/clone_lib="NCI_CGAP_Kid14"
/lab_host="DH10B" (T1 phage-resistant)"
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. |"
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                   CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9808 row: h column: 06
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Best Local Similarity 100.0%; Score 25; DB 10; Length 599;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 25; Conservative 0; Mismatches 0; Indels
issue Procurement: Jeffrey E. Green, M.D.
                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"/strain="FVB/N"/db_xref="taxon:10090"
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RESULT

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ORIGIN

SOURCE

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BB661026 RIKEN full-length enriched, 0 day neonate kidney Mus musculus cDNA clone D630017H14 5', mRNA sequence.
BB661026
                                                                                RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
10 (11), 1757-1771 (2000)
11 (11), 1757-1771 (2000)
12 and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
confocioned as sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
K. Fukuda.S. Shinaqawa.A. Saito,T. Kiyosawa.H., Yamanaka,I., Aizawa
Hayashizaki,Y.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Location/Qualifiers

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Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                  Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001) please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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/clone="E030013D02"
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5', mRNA sequence.
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Email: genome-resegsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Wormalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
wagi,K., Fullwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,M., Ohara,E.,
Na., Rawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 502)
Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
Hayatsu,N., Hiramoto,K., Hiracaha,T., Hirozaha,T.,
K., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T.,
Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T.,
Salto,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K.,
Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa
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                                                                                                                 Laboratory for Genome Exploration Research Group, RIKEN Genomic Schences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Computer based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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                                                                                                Contact: Yoshihide Hayashizaki
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Please visit our web site (http://genome.gsc.riken.go.jp) for
                        Toya, T.
                                                                                                                                                                   Contact: Yoshihide Hayashizaki
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602104020F1 NCI_CGAP_Kidl4 Mus musculus cDNA clone IMAGE:4222133
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NIH-MGC http://mgc.nci.nlh.gov/.
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Mismatches
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UKL:http://genome-gsc.riken.go.jp/
Carninci.p. K. Bayatsu.N., and Hayashizati.Y.

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sclurognathi; Muridae; Murinae; Mus.
Nammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus.
1 (bases 1 to 485)
Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T., Ishii
Hayatsu,N., Hiramcto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii
Hayatsu,N., Hiramcto,K., Nomura,K., Nonno,H., Kouda,M., Matsuyama,T.,
Y., Ito,M., Rawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T.,
Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okido,T.,
Saito,R., Sakai,C., Sakai,K., Sakazume,N., Saaski,D., Sato,K.,
Shibata,K., Shinaqawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa
,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T.
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                                                                    Unpublished (2001)
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Laboratorry for Genome Exploration Research Group, RIKEN Genomic
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                                                                                                                                                                                                                                                                      Email: genome-resegsc.riken.go.jp,
URL:http://genome-gsc.riken.go.jp,
Carninci.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
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                                                                                                                                                                          1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                              Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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/clone_lib="RIKEN full-length en
CRL-2065 MLTC-1 cDNA"
/cell_type="Leydig cells"
/cell_line="CRL-2065 MLTC-1"
a 127 c 156 g 97 t
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/db_xref="taxon:10090"
                             Unpublished (2001)
Contact: Yoshihide Hayashizaki
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BASE COUNT ORIGIN

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Query Match
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(I), MAS-1771 (2000)

Y. and Hayashizaki,Y. Shibata,K., Itch,M., Carninci,P., Sugahara Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Alzawa, M., Fukuka, S., Rara,A., Itch,M., Kawal,J., Shibata,K. and
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                                                                                                                                                                    Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                           /clone_lib="RIKEN full-length enriched, 2 days pregnant adult female ovary"
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BB863087 RIKEN full-length enriched, Leydig cells CRL-2065 MLTC-1 CDNA Mus musculus CDNA clone G430034D12 5', mRNA sequence. BB863087.1 GI:17109295
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Alakawa, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotoni, K., Ishii Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishii, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shinaqawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. 2001)
                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra MyMouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of Medicinep
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
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/clone="IMAGE:427563"
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May 23, 2002, 21:00:44 ; Search time 4203.75 Seconds (without alignments) 80.267 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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SUMMARIES

|   | Description              |               |          | -        | BB863087 BB863087 | BB857917 BB857917 | BB857913 BB857913 | BB853356 BB853356 | 000000000000000000000000000000000000000 |          | BB605812 BB605812 | BB661026 BB661026 | BB633565 BB633565 | BB650071 BB650071 | BB637089 BB637089 | BB661603 BB661603 |         | n        |            | 725967676 602799277 |          | BIDS8404 DOSSIGSS |
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|   | QI                       |               | BB666889 | AA002532 | BB863087          | BBB57917          | BB857913          | 00000000          | 000000                                  | BF780486 | BB605812          | BB661026          | BB633565          | BB650071          | BB637089          | PE661603          | COOTOGG | BB652011 | ) BE289316 | 77077004            | HG804840 | ) BI688404        |
|   | DB                       | 1             | σ        | σ        | σ                 | 0                 | 0                 | ۱ ۵               | ,                                       | 10       | 6                 | 6                 | σ                 | , σ               | ·σ                | ٥                 | ,       | σ        | 10         | 1 7                 | 7        | 10                |
|   | Query<br>Match Length DB |               | 260      | 406      | 472               | 200               | 20.0              | 000               | 700                                     | 599      | 608               | 623               | 625               | 637               | 641               | 2 7 7             | 7 70    | 649      | 651        | 1 0                 | 9//      | 779               |
| æ | Query<br>Match           |               | 100.0    | 100      | 1001              | 0.00              | 000               | 0.00              | T00.0                                   | 100.0    | 100.0             | 100               | 100               | 0.001             | 0.00              | 0.00              | T00.0   | 100.0    | 100        | 0 0                 | 100.0    | 100.0             |
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|   | ддд  | 00  | 9 BB856691<br>10 BG935945<br>9 AW889975                      | 10 BF896723<br>10 BG407897<br>9 AW245217<br>9 AW406598                               | 10 BG234205<br>9 AW630286<br>10 BE305036<br>9 AI878843                   | 9 AW629814<br>9 AW160553<br>10 BG515497<br>10 BE393833<br>9 AI690580  |
|   |  |   |  |  | 443<br>448<br>449<br>471   | 482<br>487<br>510<br>515<br>530   |
| 100.0<br>100.0<br>100.0<br>100.0  | 93.6   | 93.6<br>93.6<br>88.0  | 80.8<br>79.2<br>76.8   | 76.8<br>76.8<br>76.8   | 76.8<br>76.8<br>76.8   | 76.8<br>76.8<br>76.8<br>76.8  |
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| c 19<br>c 20<br>c 21  |  | c 26<br>c 27<br>c 28  |  | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0  |  | C 41<br>C 42<br>C 44<br>C 44  |
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## ALIGNMENTS

| BB666889 RIKEN full-length enriched, 2 days pregnant adult female covary Mus musculus cDNA clone E330035012 5', mRNA sequence. BB666889.1 GI:16500522 EST. house mouse. Mus musculus Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Sciuroqnathi; Muridae; Mus. Mus. |                      | RIKEN MOUSTINGERS (Arrkawa, T., et al. 2001) Unpublished (2001) Contact: Yoshihide Hayashizaki Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 | Email: genome_res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/ URL:http://genome.gsc.riken.go.jp/ URL:http://genome.gsc.riken.go.jp/ URL:http://genome.gsc.riken.go.jp/ URL:http://genome.gsc.riken.go.jp/ M., Konno, H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. M., Konno, H., Okazaki,Y., Muramatsu,M., Tioue,Y., Shibata, Itoh Normalizatino and subtraction of cap-trapper-selected CDNAs to subtraction and |
|---|----------------------|---|---|
| RESULT 1<br>BBE66889/C<br>LOCUS<br>LOCUS<br>DEFINITION<br>ACCESSION<br>VERSION<br>KEYWORDS<br>SOURCE<br>ORGANISM  | REFERENCE<br>AUTHORS | TITLE<br>JOURNAL<br>COMMENT   |   |